

SEQ ID NO:6 A33
 SEQ ID NO:1 40628
 SEQ ID NO:2 45416
 SEQ ID NO:9 35638
 SEQ ID NO:10 JAM

1 M V G K M W P V L W T L C A Y R Y T V D A I S V E T P Q D V L R A S Q G K S V T L P C T Y H T S T S
 1 M G T K A Q V E R K L L C L F I L A I L L C S L A L G S V T V H S S E - - - - - P E V R I P E
 1 - - - - M G I L L G L L L L G H L T V O T Y G R P I L E V P E S Y T G P W K G D V N L P C T Y O P L
 1 M A R R S R H R L L L L L R Y L V V A L G Y H K A Y G F S A P K D Q - - - - - Q V V T A V E
 1 - M G T E G K A G R K L L F L F T S M I L G S L V Q G K G S V Y T A Q - - - - - S D V Q V P E

A33 51 S R E G L I Q W D K L L L T H T E R V V I W P F S N K N Y I H G E L Y K N R V S I S N N A E Q S D A
 40628 43 N N P V K L S C A Y S G F S S P R V E W K F D Q G O T T R L V C Y N N K I T A S Y E D R V T F L P T
 45416 47 Q G Y T Q V L Y K W L Y Q R G S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P G D Y
 35638 43 Y Q E A I L A C K T P K K T V S S R L E W K K L G R S V S F V Y Y Q O T L O G D F K N R A E M I D F
 JAM 42 N E S I K L T C T Y S G F S S P R V E W K F V O G S T T A L V C Y N S Q I T A P Y A D R V T F S S S

A33 101 S I T I D O L T M A D N G T Y E C S V S L - M - - - - - S O L E G N T K S R V R L L V L V P P S K
 40628 93 G I T F K S V T R E D T G T Y T C M V S E - - - - - E G G N S Y G E V K Y K L I V L V P P S K
 45416 97 S L Q L S T L E M D D R S H Y T C E V T W O T P O G N Q V R D K I T E L R V Q K L S V S K P T V T
 35638 93 N I R I K N V T R S D A G K Y R C E V S A P S - - - - - E O G Q N L E E D T V T L E V L V A P A V
 JAM 92 G I T F S S V T R K D N G E Y T C M V S E - - - - - E G G Q N Y G E V S I H L T V L V P P S K

A33 144 P E C G I E G E T I I G H N I O L T C Q S K E G S P T P O Y S W K R Y N I L N Q E Q - - - - -
 40628 135 P T Y N I P S S A T I G N R A V L T C S E Q D G S P P S E Y T W F K D G I V M P T N - P K S T R A F
 45416 147 T G S G Y G F T V P O G M R I S L O C Q A R - G S P P I S Y I W Y K Q Q T N N Q E P - - - - -
 35638 137 P S C E V P S S A L S G T V V E L R C O D K E G N P A P E Y T W F K D G I R L L E N - P R L G S Q S
 JAM 134 P T I S V P S S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F

A33 186 - - - P L A Q P A S G Q P V S L K N I S T D T S G Y Y I C T S S N E E G - - - - - T Q F C N I T V
 40628 184 S N S S Y V L N P T T G E L V F O P L S A S D T G E Y S C E A R N G Y G - - - - - T P M T S N A V
 45416 188 - - - - I K V A T L S T L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I V K F V V K D
 35638 186 T N S S Y T M N T K T G T L O F N T V S K L D T G E Y S C E A R N S V G - - - - - Y R R C P G K R
 JAM 184 M N S S F T I D P K S G D L I F O P V T A F D S G E Y Y C Q A O N G Y G - - - - - T A M R S E A A

A33 227 A V R S P S M N V A L Y V G I A V G V Y A A L I I I G I I I Y C C C C R G K D D N T E D K E D A - -
 40628 228 R M E A V E R N V G Y I V A A V L V T L I L L G I L V F G I W F A Y S R G H F D R T K K G T S - -
 45416 233 S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W D W T T D M D G Y L G E T S A G P G K S L
 35638 230 - M Q V D D L N I S G I I A A V Y V V A L V I S V C G L G V C Y A O R K G Y F S K E T S F O K S - -
 JAM 228 H M O A V E L N V G G I Y A A V L V T L I L L G L L I F G V W F A Y S R G Y F E T T K K G T A P - -

A33 275 - R P N R E A Y E E P P E Q L R E L S R E R E E E D D Y R Q E E Q R S T G R E S P D H L O O
 40628 275 - - - - - S K K V I Y S Q P S A R S E G E F K O T S S F L V - - - - -
 45416 283 P V F A I L I I S L C C M V V F T M A Y I M L C R K T S Q O E H V Y E A A R - - - - -
 35638 277 - N S S S K A T T M - S E N V Q W L T P V I P A L W K A A A G G S R G Q E F - - - - -
 JAM 276 - - - - - G K K V I Y S Q P S T R S E G E F K O T S S F L V - - - - -

Figure 1

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile Leu Ala Ile Leu Cys Ser Leu Ala Leu Gly Ser Val Thr	1	5	10	15	20	25	30
Val His Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val	35	40	45	50	55	60	65
Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu	65	70	75	80	85	90	95
Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Asn Ser Tyr Gly	95	100	105	110	115	120	125
Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val	125	130	135	140	145	150	155
Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr	155	160	165	170	175	180	185
Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr	185	190	195	200	205	210	215
Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val	215	220	225	230	235	240	245
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys	245	250	255	260	265	270	275
Lys Gly Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val	275	280	285	290	295	300	305

Figure 2

1 MGILLGLLLL GHLTVDTYGR PILEVPESVT GPWKGDVNL P CTYDPLQGYT QVLVKWLVQR GSDPVTIFLR DSSGDHIQQA KYQGRHLHVSH KVPGDVSLQL

101 STLEMDDRRSH YTCEVTWQTP DGNQVVRDKI TELRVQKLSV SKPTVTTCSG YGFTVPQGM R ISLQCQARGS PPISYIWKQ QTNNOEPIKV ATLSTLLFKP

201 AVIADSGSYF CTAKGQVGSE QHSDIVKVV KDSSKLLKTK TEAPTTMTYP LKATSTVKQS WDWTDDMDGY LGETSAGPGK SLPVFAILI ISLCCMVVFT

301 MAYIMLCRKT SQQEHVYEA R

^Glycosaminoglycan attachment site

^Transmembrane domain

Figure 3

DNA35936 (SEQ ID NO: 3)

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CTTCTTGCCA ACTGGTATCA CCTTCAAGTC CGTGACACGG GAAGACACTG 50
GGACATACAC TTGTATGGTC TCTGAGGAAG GCGGCAACAG CTATGGGGAG 100
GTCAAGGTCA AGCTCATCGT GCTTGTGCCT CCATCCAAGC CTACAGTTAA 150
CATCCCCTCC TCTGCCACCA TTGGGAACCG GGCAGTGCTG ACATGCTCAG 200
AACAAGATGG TTCCCCACCT TCTGAATACA CCTGGTTCAA AGATGGGATA 250
GTGATGCCTA CGAATCCCAA AAGCACCCGT GCCTTCAGCA ACTCTTCCTA 300
TGTCTGAAT CCCACAACAG GAGAGCTGGT CTTTGATCCC CTGTCAGCCT 350
CTGATACTGG AGAATACAGC TGTGAGGCAC GGAATGGGTA 390

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Figure 4A

consen01 (SEQ ID NO: 4)

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TCTCAGTCCC CTCGCTGTAG TCGCGGAGCT GTGTTCTGTT TCCCAGGAGT 50
CCTTCGGCGG CTGTTGTGCT CAGGTGCGCC TGATCGCGAT GGGGACAAAG 100
GCGCAAGCTC GAGAGGAAAC TGTTGTGCCT CTTCATATTG GCGATCCTGT 150
TGTGCTCCCT GGCATTGGGC AGTGTTACAG TTGCACTCTT CTGAACCTGA 200
AGTCAGAATT CCTGAGAATA ATCCTGTGAA GTTGTCCTGT GCCTACTCGG 250
GCTTTTCTTC TCCCCGTGTG GAGTGGAAGT TTGACCAAGG AGACACCACC 300
AGACTCGTTT GCTATAATAA CAAGATCACA GCTTCCTATG AGGACCGGGT 350
GACCTTCTTG CCAACTGGTA TCACCTTCAA GTCCGTGACA CGGGAAGACA 400
CTGGGACATA CACTTGTATG GTCTCTGAGG AAGGCGGCAA CAGCTATGGG 450
GAGGTCAAGG TCAAGCTCAT CGTGCTTGTG CCTCCATCCA AGCCTACAGT 500
TAACATCCCC TCCTCTGCCA CCATTGGGAA CCGGGCAGTG CTGACATGCT 550
CAGAACAAGA TGGTTCCCCA CCTTCTGAAT ACACCTGGTT CAAAGATGGG 600
ATAGTGATGC CTACGAATCC CAAAAGCACC CGTGCCTTCA GCAACTCTTC 650
CTATGTCCTG AATCCCACAA CAGGAGAGCT GGTCTTTGAT CCCCTGTCAG 700
CCTCTGATAC TGGAGAATAC AGCTGT 726

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Figure 4B

consen02 (SEQ ID NO:5)

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GCAGGCAAAG TACCAGGGCC GCCTGCATGT GAGCCACAAG GTTCCAGGAG 50
ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC 100
ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCAACCAAG TCGTGAGAGA 150
TAAGATTACT GAGCTCCGTG TCCAGAAACT CTCTGTCTCC AAGCCCACAG 200
TGACAACTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT 250
AGCCTTCAAT GCCAGGGTTC GGGGTTCCTCC TCCCATCAGT TATATTTGGT 300
ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCCTAAG 350
TACCTTACTC TTCAAGCCTG CGGTGATAGC CGACTCAGGC TCCTATTTCT 400
GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCACAGCGA CATTGTGAAG 450
TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC 500
TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT 550
GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGGG 600
CCAGGAAAGA GCCTGCCTGT CTTTGCCATC ATCCTCATCA TCTCCTTGTG 650
CTGTATGGTG GTTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT 700
CCCAACAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC 750
AACGACTCTG GAGAAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC 800
CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAATA CTCTGATGAG 850
CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA 900
CGCCCGCCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG 950
AGGGCAAAAG TGTCTGTTAA AAATGCCCCA TTAGGCCAGG ATCTGCTGAC 1000
ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC 1050
CTCTCTTCCT GGATAGCCCA AAGTGTCCGC CTACCAACAC TGGAGCCGCT 1100
GGGAGTCACT GGCTTTGCCC TGGAATTTGC CAGATGCATC TCAAGTAAGC 1150
CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT 1200
CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCATA GCACTAGGAC 1250
TTGGTCATCA TGCCTACAGA CACTATTCAA CTTTGGCATC TTGCCACCAG 1300
AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC 1350
CAGGATCATT TCTCTTTCTT CAGGGCCAGA CAGCTTTTAA TTGAAATTGT 1400
TATTTACAG GCCAGGGTTC AGTTCTGCTC CTCCACTATA AGTCTAATGT 1450
TCTGACTCTC TCCTGGTGCT CAATAAATAT CTAATCATAA CAGCAAAAAA 1500
AAA 1503
```

Figure 4C

SEQ ID NO:11

GTCTGTTCCC (AGGAGTCCCTT CGCGGGCTGT TGTGTCAGTG GCCTGATCGC GATGGGGACA AAGGCGCAAG TCGAGAGGAA ACTGTTGTGC CTCTTCATAT 100
TGGCGATCCT GTTGTGCTCC CTGGCATGG GCAGTGTTAC AGTGCACTCT TCTGAACCTG AAGTCAGAAT TCCTGAGAAT AATCCTGTGA AGTTGTCCTG 200
TGCCTACTCG GGCCTTTCTT CTCCCCGTGT GGAGTGGAAG TTGACCAAG GAGACACCAC CAGACTCGTT TGCTATAATA ACAAGATCAC AGCTTCCTAT 300
GAGGACCGGG TGACCTTCTT GCCAACTGGT ATCACCTTCA AGTCCGTGAC ACGGGAAGAC ACTGGGACAT ACACCTTGAT GGTCTCTGAG GAAGGCGGCA 400
ACAGCTATGG GGAGGTCAAG GTCAAGCTCA TCGTGCTTGT GCCTCCATCC AAGCCTACAG TTAACATCCC CTCCTCTGCC ACCATTGGGA ACCGGGCAGT 500
GCTGACATGC TCAGAACAAG ATGGTTCCCC ACCTTCTGAA TACACCTGGT TCAAAGATGG GATAGTGATG CCTACGAATC CCAAAGGCAC CCGTGCCTTC 600
AGCAACTCTT CCTATGTCCT GAATCCCACA ACAGGAGAGC TGGTCTTTGA TCCCCTGTCA GCCTCTGATA CTGGAGAATA CAGCTGTGAG GCACGGAATG 700
GGTATGGGAC ACCCATGACT TCAAATGCTG TGCGCATGGA AGCTGTGGAG CGGAATGTGG GGGTCATCGT GGCAGCCGTC CTTGTAACCC TGATTCTCCT 800
GGGAATCTTG GTTTTTGGCA TCTGGTTTGC CTATAGCCGA GGCCACTTTG ACAGAACAAA GAAAGGGACT TCGAGTAAGA AGGTGATTTA CAGCCAGCCT 900
AGTGCCCGAA GTGAAGGAGA ATTCAAACAG ACCTCGTCAT TCCTGGTGTG AGCCTGGTCG GCTCACCGCC TATCATCTGC ATTTGCCTTA CTCAGGTGCT 1000
ACCGGACTCT GGCCCCTGAT GTCTGTAGTT TCACAGGATG CCTTATTGT CTTCTACACC CCACAGGGCC CCCTACTTCT TCGGATGTGT TTTTAATAAT 1100
GTCAGCTATG TGCCCCATCC TCCTTCAIGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG GCCTGGAAC TGTTTAAAGT GTTTATTCCC CATTTCCTTG 1200
AGGGATCAGG AAGGAATCCT GGGTATGCCA TTGACTTCCC TTCTAAGTAG ACAGCAAAA TGGCGGGGT CGCAGGAATC TGCACCTCAAC TGCCCACCTG 1300
GCTGGCAGGG ATCTTTGAAT AGGTATCTTG AGCTTGGTTC TGGGCTCTTT CCTTGTGTAC TGACGACCAG GGCCAGCTGT TCTAGAGCGG GAATTAGAGG 1400
CTAGAGCGGC TGAATGGTT GTTTGGTGAT GACACTGGG TCCTTCCATC TCTGGGCCC ACTCTCTTCT GTCTTCCCAT GGGAAAGTGCC ACTGGGATCC 1500
CTCTGCCCTG TCCTCCTGAA TACAAGCTGA CTGTGCTGT GGAATGGG AGCTCTTGT GTGGAGAGCA TAGTAAATTT TCAGAGAACT 1600
TGAAGCCAAA AGGATTTAAA ACCGCTGCTC TAAAGAAAAG AAAACTGGAG GCTGGGCGCA GTGGCTCAGG CCTGTAATCC CAGAGGCTGA GGCAGGCGGA 1700
TCACCTGAGG TCGGGAGTTC GGGATCAGCC TGACCAACAT GGAGAAACCC TACTGGAAT ACAAGTTAG CCAGGCATGG TGGTGCATGC CTGTAGTCCC 1800
AGCTGCTCAG GAGCCTGGCA ACAAGAGCAA AACTCCAGCT CA 1842

Figure 5

SEQ ID NO:7

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1 CCCACGGCTC CGCCACGGC TCCGCCACG GGTCCGCCA CGCTCCGGG CCACCAGAAG TTTGAGCCTC TTTGGTAGCA GGAGGCTGGA AGAAAGGACA
GGGTGCCGAG GCGGGTGCGC AGCGGGGTGC CCAGGGGGGT GCGCAGGCC CCAGGGGGGT AAACCTCGGAG AAACCATCGT CCTCCGACCT TCTTCCCTGT

101 GAAGTAGCTC TGGCTGTGAT GGGGATCTTA CTGGGCCTGC TACTCCTGGG GCACCTAACA GTGGACACTT ATGGCCGTCC CATCCTGGAA GTGCCAGAGA
CTTCATCGAG ACCGACACTA CCCCTAGAAAT GACCCGGAGC ATGAGGACCC CGTGGATTGT CACCTGTGAA TACCGGCAGG GTAGGACCTT CACGGTCTCT

1 SEQ ID NO:2 M G I L L G L L L G L L G H L T V D T Y G R P I L E V P E S
^MET

201 GTGTAACAGG ACCTTGGAAA GGGGATGTGA ATCTTCCCTG CACCTATGAC CCCCTGCAAG GCTACACCCA AGTCTTGGTG AAGTGGCTGG TACAACGTGG
CACATTGTCC TGGAACTTTT CCCCTACACT TAGAAGGGAC GTGGATACTG GGGGACGTTT CGATGTGGT TCAGAACCAC TTCACCGACC ATGTTGCACC

29 V T G P W K G D V N L P C T Y D P L Q G Y T Q V L V K W L V Q R G

301 CTCAGACCCCT GTCACCATCT TTCTACGTGA CTCTTCTGGA GACCATATCC AGCAGGCAAA GTACCAGGC CCGCTGCATG TGAGCCACAA GGTTCACAGG
GAGTCTGGGA CAGTGGTAGA AAGATGCACT GAGAAGACCT CTGCTCGTTT CATGGTCCCG CCGGACGTAC ACTCGGTCTT CCAAGGTCTT

62 S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P G

401 GATGTATCCC TCCAATTGAG CACCCTGGAG ATGGATGACC GGAGCCACTA CACGTGTGAA GTCACCTGGC AGACTCCTGA TGGCAACCAA GTCGTGAGAG
CTACATAGGG AGGTTAACTC GTGGGACCTC TACCTACTGG CCTCGGTGAT GTGCACACTT CAGTGGACCG TCTGAGGACT ACCGTTGGTT CAGCACTCTC

95 D V S L Q L S T L E M D D R S H Y T C E V T W Q T P D G N Q V V R D

501 ATAAGATTAC TGAGCTCCGT GTCCAGAAAC TCTCTGCTC CAAGCCCACA GTGACAACTG GCAGCGGTTA TGGCTTCAGG GTGCCCCAGG GAATGAGGAT
TATTCTAATG ACTCGAGGCA CAGGTCTTTG AGAGACAGAG GTTCGGGTGT CACTGTTGAC CGTCGCCAAT ACCGAAAGTC CACGGGGTCC CTTACTCCTA

129 K I T E L R V Q K L S V S K P T V T T G S G Y G F T V P Q G M R I

601 TAGCCTTCAA TGCCAGGCTC GGGGTTCTCC TCCCATCAGT TATATTGGT ATAAGCAACA GACTAATAAC CAGGAACCCA TCAAAGTAGC AACCTTAAGT
ATCGGAAGTT ACGGTCCGAG CCCCAAGAGG AGGTTAGTCA ATATAAACCA TATTCTGTTG CTGATTATTG GTCCTTGGGT AGTTTCATCG TTGGGATTCA

162 S L Q C Q A R G S P P I S Y I W Y K Q Q T N N Q E P I K V A T L S

701 ACCTTACTCT TCAAGCCTGC GGTGATAGCC GACTCAGGCT CCTATTCTG CACTGCCAAG GCCCAGGTTG GCTCTGAGCA GCACAGCGAC ATTGTGAAGT
TGGAATGAGA AGTTCGGACG CCACTATCGG CTGAGTCCGA GGATAAAGAC GTGACGGTTC CCGGTCCAAC CGAGACTCGT CGTGTGCTG TAACACTTCA

195 T L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I V K F

801 TTGTGGTCAA AGACTCCTCA AAGCTACTCA AGACCAAGAC TGAGGCACCT ACAACCATGA CATACCCCTT GAAAGCAACA TCTACAGTGA AGCAGTCCTG
AACACCAAGT TCTGAGGAGT TTCGATGAGT TCTGGTTCTG ACTCCGTGGA TGTTGGTACT GTATGGGAA CTTTCTGTGT AGATGTCACT TCGTCAGGAC

229 V V K D S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W
```

Figure 6A

SEQ ID NO:7	901	GGACTGGACC	ACTGACATGG	ATGGCTACCT	TGGAGAGACC	AGTGCTGGGC	CAGGAAAGAG	CCTGCCTGTC	TTTGCCATCA	TCCTCATCAT	CTCCTTGTGC
		CCTGACCTGG	TGACTGTACC	TACCGATGGA	ACCTCTCTGG	TCACGACCCG	GTCTTTCTC	GGACGGACAG	AAACGGTAGT	AGGAGTAGTA	GAGGAACACG
SEQ ID NO:2	262	D W T	T D M	D G Y L	G E T	S A G P	G K S	L P V	F A I I	L I I	S L C
	1001	TGTATGGTGG	TTTTTACCAT	GCCCTATATC	ATGCTCTGTC	GGAAGACATC	CCAACAAGAG	CATGCTCTACG	AAGCAGCCAG	GTAAGAAAGT	CTCTCCTCTT
		ACATACCACC	AAAATGGTA	CCGGATATAG	TACGAGACAG	CCTTCTGTAG	GGTTGTTCTC	GTACAGATGC	TTCGTCCGTC	CATTCTTTCA	GAGAGGAGAA
	295	C M V V	F T M	A Y I	M L C	R K T	S Q Q	E H V	Y E A	A R O	
	1101	CCATTTTGA	CCCCGTCCCT	GCCCTCAATT	TTGATTACTG	GCAGGAAATG	TGGAGGAAGG	GGGGTGTGGC	ACAGACCCAA	TCCTAAGGCC	GGAGGCCCTTC
		GGTAAAAACT	GGGGCAGGGA	CGGGAGTTAA	AACATAAGAC	CGTCTTTTAC	ACCTCCTTCC	CCCCACACCG	TGCTGGGTT	AGGATTCCGG	CCTCCCGAAG
	1201	AGGGTCAGGA	CATAGCTGCC	TTCCCTCTCT	CAGGCACCTT	CTGAGGTTGT	TTTGGCCCTC	TGAACACAAA	GGATAATTTA	GATCCATCTG	CCTTCTGCTT
		TCCCAGTCCT	GTATCGACGG	AAGGGAGAGA	GTCCGTGGAA	GACTCCAACA	AAACCCGGAG	ACTTGTGTTT	CCTATTAAAT	CTAGGTAGAC	GGAAGACGAA
	1301	CCAGAAATCC	TGGGTGGTAG	GATCCTGATA	ATTAATTGGC	AAGAATTGAG	GCAGAAAGGT	GGGAAACCAG	GACCACAGCC	CCAAGTCCCT	TCTTATGGGT
		GGTCTTAGGG	ACCCACCATC	CTAGGACTAT	TAATTAACCG	TTCTTAACTC	CGTCTTCCCA	CCCTTTGGTC	CTGGTCTCGG	GGTTCAGGGA	AGAATACCCA
	1401	GGTGGGCTCT	TGGGCCATAG	GGCACATGCC	ACGACTCTGG	AGAAACCATG	AGGGTGGCCA	TCTTCGGCAAG	TGGCTGCTCC	AGTGATGAGC	
		CCACCCGAGA	ACCCGGTATC	CCGTGTACGG	TCTCTCCGGT	TGCTGAGACC	TCTTTGGTAC	TCCCACCGGT	AGAAGCGTTC	ACCGACGAGG	TCACTACTCG
	1501	CAACTTCCCA	GAATCTGGGC	AACAATACT	CTGATGAGCC	CTGCATAGGA	CAGGAGTACC	AGATCATCGC	CCAGATCAAT	GGCAACTACG	CCCGCCCTGCT
		GTTGAAGGGT	CTTAGACCCG	TTGTTGATGA	GACTACTCGG	GACGTATCCT	GTCTCATCGG	TCTAGTAGCG	GGTCTAGTTA	CCGTTGATGC	GGCGCGACGA
	1601	GGACACAGTT	CCCTCTGGATT	ATGAGTTTCT	GGCCACTGAG	GGCAAAAGTG	TCTGTTAAAA	ATGCCCCCATT	AGGCCAGGAT	CTGCTGACAT	AATTGCCTAG
		CCTGTGTCAA	GGAGACCTAA	TACTCAAAGA	CCGGTGACTC	CCGTTTTTAC	AGACAATTTT	TACGGGGTAA	TCCGGTCCCTA	GACGACTGTA	TTAACGGGATC
	1701	TCAGTCCCTG	CCTTCTGTCAT	GGCCTTCTTC	CCTGTCTACCT	CTCTTCTCTG	ATAGCCCCAA	GTGTCCGCCT	ACCAACACTG	GAGCCGCTGG	GAGTCACTGG
		AGTCAGGAAC	GGAAGACGTA	CCGGAAGAAG	GGACGATGGA	GAGAAGGACC	TATCGGGTTT	CACAGGCGGA	TGGTTGTGAC	CTCGGCGACC	CTCAGTGACC
	1801	CTTTGCCCTG	GAATTTGCCA	GATGCATCTC	AAGTAAGCCA	GCTGTGGGAT	TTGGCTCTGG	GCCCTTCTAG	TATCTCTGCC	GGGGGCTTCT	GGTACTCCTC
		GAAACGGGAC	CTTAAACGGT	CTACGTAGAG	TTCATTCCGT	CGACGACCTA	AACCGAGACC	CGGGAAGATC	ATAGAGACGG	CCCCCGAAGA	CCATGAGGAG
	1901	TCTAAATACC	AGAGGGAAGA	TGCCCATAGC	ACTAGGACTT	GGTCATCATG	CCTACAGACA	CTATTCAACT	TTGGCATCTT	GCCACCAGAA	GACCCGAGGG
		AGATTTATGG	TCTCCCTTCT	ACGGGTATCG	TGATCCTGAA	CCAGTAGTAC	GGATGTCTGT	GATAAGTTGA	AACCGTAGAA	CGGTGGTCTT	CTGGGCTCCC
	2001	AGGCTCAGCT	CTGCCAGCTC	AGAGGACCAG	CTATATCCAG	GATCATTTCT	CTTTCTTCAG	GGCCAGACAG	CTTTTAATTG	AAATTGTTAT	TTCACAGGCC
		TCCGAGTCGA	GACGGTCGAG	TCTCCTGGTC	GATATAGGTC	CTAGTAAAGA	GAAAGAAGTC	CCGGTCTGTC	GAAAAATTAAC	TTTAACAATA	AAGTGTCGGG
	2101	AGGGTTCAGT	TCTGCTCCTC	CACTATAAGT	CTAATGTTCT	GACTCTCTCC	TGGTGCTCAA	TAAATATCTA	ATCATAACAG	C	
		TCCCAAGTCA	AGACGAGGAG	GTGATATTCA	GATTACAAGA	CTGAGAGAGG	ACCACGAGTT	ATTTATAGAT	TAGTATTGTC	G	

Figure 6B

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCT
CAGAGCAGCCGGCTGCCGCCCGGGAAGATGGCGAGCAGGAGCCGCCACCGCCTCCTCCT
GCTGCTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGC
CCCAAAGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAA
AACCCCAAAGAAGACTGTTTCCTCCAGATTAGAGTGGAAGAACTGGGTCGGAGTGTCTC
CTTTGTCTACTATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGA
TTTCAATATCCGGATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGT
TAGTGCCCATCTGAGCAAGGCCAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATT
AGTGGCTCCAGCAGTTCCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGT
AGAGCTACGATGTCAAGACAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTTAAGGA
TGGCATCCGTTTGCTAGAAAATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACAC
AATGAATACAAAACCTGGAAGTCTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGA
ATATTCCTGTGAAGCCCGCAATTCTGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCA
AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGAT
TTCCGTTTGTGGCCTTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTTCAAAGAAAC
CTCCTTCCAGAAGAGTAATTCTTCATCTAAAGCCACGACAATGAGTGAAAATGTGCAGTG
GCTCACGCCTGTAATCCCAGCACTTTGGAAGGCCGCGGCGGGCGGATCACGAGGTCAGGA
GTTCTAGACCAGTCTGGCCAATATGGTGAAACCCCATCTCTACTAAAATACAAAATTAG
CTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGCTTGGGAGACAGGAGAATCACTTGA
ACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGCCACTGCAGTCCAGCCTGGGTAA
CAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATAAATAAATAAATAAATAAATAA
TGTAGAATTCTTACAATAAATATAGCTTGATATTC

Figure 7

OLI2162 (35936.f1)
SEQ ID NO:12

TCGCGGAGCTGTGTTCTGTTTCCC

OLI2163 (35936.p1)
SEQ ID NO:13

TGATCGCGATGGGGACAAAGGCGCAAGCTCGAGAGGAAACTGTTGTGCCT

OLI2164 (35936.f2)
SEQ ID NO:14

ACACCTGGTTCAAAGATGGG

OLI2165 (35936.r1)
SEQ ID NO:15

TAGGAAGAGTTGCTGAAGGCACGG

OLI2166 (35936.f3)
SEQ ID NO:16

TTGCCTTACTCAGGTGCTAC

OLI2167 (35936.r2)
SEQ ID NO:17

ACTCAGCAGTGGTAGGAAAG

Figure 8

SEQ ID NO:5

1 GCAGGCAAG TACCAGGGCC GCCTGCATGT GAGCCACAAG GTTCCAGGAG ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC
CGTCCGTTTC ATGGTCCCG CGGACGTACA CTCGGTGTTC CAAGGTCTC TACATAGGA GGTAACTCG TGGACCTCT ACCTACTGGC CTCGGTGATG

^42257.f1 SEQ ID NO:18 ^42257.p1 SEQ ID NO:22

101 ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCAACCAAG TCGTGAGAGA TAAGATTACT GAGCTCCGTG TCCAGAAACT CTCTGTCTCC AAGCCACAG
TGCACACTTC AGTGGACCGT CTGAGGACTA CCGTTGGTTC AGCACTCTCT ATTCTAATGA CTCGAGGCAC AGGTCTTTGA GAGACAGAGG TTCCGGGTGTC

201 TGACAACTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT AGCCTTCAAT GCCAGGGTTC GGGGTTCTCC TCCCATCAGT TATATTTGGT
ACTGTTGACC GTCGCCAATA CCGAAGTGCC ACGGGGTCCC TTA CTCTCTAA TCGGAAGTTA CCGTCCCAAG CCCCAGAGG AGGTAGTCA ATATAAACCA

301 ATAAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCCCTAAG TACCTTACTC TTCAAAGCCTG CCGTGATAGC CGACTCAGGC TCCTATTTCT
TATTCGTTGT CTGATTATTG GTCCCTTGGG TAGTTTCATC GTTGGGATTC ATGGAATGAG AAGTTCGGAC GCCACTATCG GCTGAGTCCG AGGATAAAGA

401 GCACTGCCAA GGGCCAGGTT GGCTCTGACC AGCACAGCGA CATTGTGAAG TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC
CGTGACGGTT CCGGTCCAA CCGAGACTCG TCGTGTCGCT GTAACACTTC AAACACCACT TTCTGAGGAG TTTCGATGAG TTCTGGTTCT GACTCCGTTGG

^42257.r1 SEQ ID NO:20

501 TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCTT GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTCTGGG
ATGTTGGTAC TGTATGGGA ACTTTCGTTG TAGATGTCAC TTCGTCAGGA CCTGACCTG GTGACTGTAC CTACCGATGG AACCTCTCTG GTCACGACCC

601 CCAGGAAGA GCCTGCCTGT CTTTGCCATC ATCCTCATCA TCTCCTTGTG CTGTATGGTG GTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT
GGTCCCTTCT CGGACGGACA GAAACGGTAG TAGGAGTAGT AGAGGAACAC GACATACCAC CAAAATGGT ACCGGATATA GTACGAGACA GCCTTCTGTA

^42257.f2 SEQ ID NO:19

701 CCCAACAAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC AAGCACTCTG GAGAAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC
GGGTGTTCT CGTACAGATG CTTCTGTCGGT CCGGTGTACG GTCTCTCCGG TTGCTGAGAC CTCCTTGGTA CTCGCCCGG TAGAAGCGTT CACCGACGAG

801 CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAAC TA CTCTGATGAG CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA
GTCAC TACTC GGTGAAGG TCTTAGACCC CGTTGTTGAT GAGACTACTC GGGACCTATC CTGTCCTCAT GGTCTAGTAG CCGGTCTAGT TACCGTTGAT

901 CGCCCCGCTG CTGGACACAG TTCCTCTGGA TTATGAGTTT CTGGCCACTG AGGCCAAAG TGTCTGTAA AAATGCCCA TTAGGCCAGG ATCTGCTGAC
GCGGGGGGAC GACCTGTGTC AAGGAGACCT AATACTCAA GACCGGTGAC TCCCGTTTC ACAGACAATT TTTACGGGGT AATCCGGTCC TAGACGACTG

1001 ATAATTGCCT AGTCAGTCTT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC CTCTCTTCTT GATAGCCCA AAGTGTCCGC CTACCAACAC TGGAGCCGCT
TATTAACGGA TCAGTCAGGA ACGGAAGACG TACCGGAAGA AGGGACGATG GAGACAAGGA CCTATCGGGT TTCACAGGCG GATGGTTGTG ACCTCGGCGA

Figure 9A

SEQ ID NO:5

1101 GGGAGTCACT GGCTTTGCC TGAATTTC CAGATGCATC TCAAGTAAGC CAGCTGCTGG ATTTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT
CCCTCAGTGA CCGAAACGGG ACCTTAAACG GTCTACGTAG AGTTCATTCTG GTCGACGACC TAAACCGAGA CCCGGGAAGA TCATAGAGAC GGCCCCCGAA
~42257.r2 SEQ ID NO:21

1201 CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCCCATA GCACTAGGAC TTGGTCATCA TGCCTACAGA CACTATTCAA CTTTGGCATC TTGCCACCAG
GACCATGAGG AGAGATTTAT GGTCTCCCTT CTACGGGTAT CGTGATCCTG AACCAGTAGT ACGGATGTCT GTGATAAGTT GAAACCGTAG AACGGTGGTC

1301 AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC CAGGATCATT TCTCTTTCTT CAGGGCCAGA CAGCTTTTAA TTGAAATTGT
TTCTGGGCTC CCCTCCGAGT CGAGACGGTC GAGTCTCCTG GTCGATATAG GTCCTAGTAA AGAGAAAGAA GTCCCGGTCT GTCGAAATTT AACTTTAACA

1401 TATTTACAG GCCAGGGTTC AGTCTGCTC CTCCACTATA AGTCTAATGT TCTGACTCTC TCCTGGTGCT CAATAAATAT CTAATCATAA CAGCAAAAA
ATAAAGTGT CCGTCCCAAG TCAAGACGAG GAGGTGATAT TCAGATTACA AGACTGAGAG AGGACCACGA GTTATTTATA GATTAGTATT GTCGTTTTTT

1501 AAA
TTT

Figure 9B

			Frame	Score	Match	Pct
A33_human	A33 antigen precursor - Homo sapiens		+1	246	81	30
A33_human - A33 antigen precursor - Homo sapiens (319 aa) Score = 246 (86.6 bits), Expect = 2.8e-19, P = 2.8e-19 Identities = 81/268 (30%), Positives = 131/268 (48%), at 121,17, Frame = +1						
DNA40628	121	LALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPR---VEW-KFDQGDTRLVC--YNN				
SEQ ID NO:23	 * . . . * . * * * * . * * . . * * . * * . . *				
A33_human	17	VTVD AISVETPQDVL RASQGKSVTL PCTYHTSTSSREGLIQWDKLLLTHTERVVIWPFSN				
SEQ ID NO:24						
DNA40628	283	K--ITAS-YEDRVTF L-----PTGITFKSVTREDTGTYTCMVS---EEGGNSYGEVKVK				
		* * * . . * * . * * * * * * * * . * * . . *				
A33_human	77	KNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVSLMSDLEGNT--KSRVR				
DNA40628	427	LIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSN				
		* . * * * * * * * * * * * * * . * * . *				
A33_human	135	LLVLVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQP-----				
DNA40628	607	SSYVLNPTTGELV-FDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGV---IVA				
		. * . * . * . * . * * * . * * . * * . *				
A33_human	187	---LAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNVALYVGIAV				
DNA40628	775	AVLVTLILLGILVFGIWFAYS RGHFDRT--KKG TSSKKVIYSQP				
		* . * * . * * * * * * * * . * * . *				
A33_human	244	GVVAALIIIGIIIIY---CCCCRGKDDNTEDKEDARPNREAYEEP				

Figure 10A

Score = 245 (86.2 bits), Expect = 3.6e-19, P = 3.6e-19
 Identities = 83/273 (30%), Positives = 131/273 (47%), at 112,12, Frame = +1

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DNA40628  112  LCSL--ALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPR---VEW-KFDQGDTTTRLVC
SEQ ID NO:25
          **.. . . . * . . . * . . . * * * * . * * . . * * . * * . *
A33_human  12  LCAVRVTVDIAISVETPQDVLRA SQGKSVTLPC TYHTSTSSREGLIQWDKLLLTHTERVVI
SEQ ID NO:26

DNA40628  274  --YNNK--ITAS-YEDRVTF L-----PTGITFKSVTREDTGTYTCMVSEEGGNSYGEVK
          ..** * . . . * . . . . . . . . . . . . . . . . . . . . . . .
A33_human  72  WPFSNKNYIHGELYKNRVSI SNNAEQSDASITIDQLTMADNGTYECSVSLMS-DLEGNTK

DNA40628  421  --VKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTR
          * . * . * * * * * * * . . . . . . . . . . . . . . . . . . .
A33_human  131 SRVRLLVLVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQP----

DNA40628  595  AFSNSSYVLNPTTGELV-FDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGV--
          . * . * . * . . . * . . . * * * . . . * . . . * * .
A33_human  187  -----LAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSMNVALYV

DNA40628  766  -IVAAVLVTLILLGILVFGIWFAYS RGHFDRT--KKGTSSKKVIYSQP
          * . * . * * . . . . . . . . . . . . . . . . . . . . . .
A33_human  240  GIAVGVAALIIIGIIIIY---CCCCRGKDDNTEDKEDARPNREAYEEP

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Figure 10B

SEQ ID NO:9

MARRSRHRLLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSR
LEWKKLGRSVSFVYYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPR
LGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYYRRCPGKRMQVDDLNISGI
IAAVVVVALVISVCGLGVCYAQRKGYFSKETSFQKSNSSSSKATTMSENVQWLTPVIPALW
KAAAGGSRGQEF

Figure 11

SEQ ID NO:6	A33_hum	1	M	V	G	K	M	W	P	V	L	W	T	L	C	A	V	R	V	T	V	D	A	I	S	V	E	T	P	O	D	V	L	R	A	S	O	G	K	S	V	T	L								
SEQ ID NO:1	40628	1	M	G	T	K	A	O	V	E	R	K	L	L	C	L	F	I	L	A	I	L	L	C	S	-	-	L	A	L	G	S	V	T	V	H	S	S	E	P	E	V	R	I	P	E	N	N	P	V	K	L
A33_hum	40628	42	P	C	T	Y	H	T	S	T	S	S	R	E	G	L	I	O	W	D	K	L	L	T	H	T	E	R	V	V	I	W	P	F	S	N	K	N	Y	I	H	G	E	L	Y	K	N	R	V	S	I	
		49	S	C	A	Y	S	G	F	S	S	P	R	-	-	-	V	E	W	-	K	F	D	O	G	D	T	T	R	L	V	C	-	-	Y	N	K	-	-	I	T	A	S	-	Y	E	D	R	V	T	F	
A33_hum	40628	92	S	N	N	A	E	O	S	D	A	S	I	T	I	D	O	L	T	M	A	D	N	G	T	Y	E	C	S	V	S	L	M	S	D	L	E	G	N	T	K	S	R	V	R	L	L	V	L	V	P	P
		90	-	-	-	-	-	L	P	T	G	I	T	F	K	S	V	T	R	E	D	T	G	T	Y	T	C	M	V	S	E	E	G	-	N	S	Y	G	E	V	K	V	K	L	I	V	L	V	P	P		
A33_hum	40628	142	S	K	P	E	C	G	I	E	G	E	T	I	I	G	N	N	I	O	L	T	C	O	S	K	E	G	S	P	T	P	O	Y	S	W	K	R	Y	N	I	L	N	Q	E	O	P	-	-	-	-	
		133	S	K	P	T	V	N	I	P	S	S	A	T	I	G	N	R	A	V	L	T	C	S	E	O	D	G	S	P	P	S	E	Y	T	W	F	K	D	G	I	V	M	P	T	N	P	K	S	T	R	A
A33_hum	40628	187	-	-	-	-	-	L	A	O	P	A	S	G	O	P	V	S	L	K	N	I	S	T	D	T	S	G	Y	Y	I	C	T	S	S	N	E	E	G	T	O	F	C	N	I	T	V	A	V	R	S	
		183	F	S	N	S	S	Y	V	L	N	P	T	T	G	E	-	L	V	F	D	P	L	S	A	S	D	T	G	E	Y	S	C	E	A	R	N	G	Y	G	T	P	M	T	S	N	A	V	R	M	E	A
A33_hum	40628	231	P	S	M	N	V	A	L	Y	V	G	I	A	V	G	V	V	A	A	L	I	I	I	G	I	I	I	Y	C	C	-	C	C	R	G	K	D	D	N	T	E	D	K	E	D	A	R	P	N	R	E
		232	V	E	R	N	V	G	V	-	-	-	I	V	A	A	V	L	V	T	L	I	L	L	G	I	L	V	F	G	I	W	F	A	Y	S	R	G	H	F	D	R	T	K	K	G	T	S	S	K	K	V
A33_hum	40628	280	A	Y	E	E	P	P	E	O	L	R	E	L	S	R	E	R	E	E	E	D	D	Y	R	O	E	E	O	R	S	T	G	R	E	S	P	D	H	L	D	O										
		279	I	Y	S	O	P	S	A	R	S	E	G	E	F	K	O	T	S	S	F	L	V																													

Figure 12

SEQ ID NO:6 A33_hum
SEQ ID NO:2 45416

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Figure 13

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SEQ ID NO:9 35638

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Figure 14

SEQ ID NO:10 jam
SEQ ID NO:1 40628

jam	1	M	G	T	E	G	K	A	G	R	K	L	L	F	L	F	T	-	S	M	I	L	G	S	L	V	O	G	K	G	S	V	Y	T	A	O	S	D	V	O	V	P	E	N	E	S	I	K	L	T	C
40628	1	M	G	T	K	A	O	V	E	R	K	L	L	C	L	F	I	L	A	I	L	L	C	S	L	A	L	G	S	V	T	V	H	S	S	E	P	E	V	R	I	P	E	N	N	P	V	K	L	S	C
jam	50	T	Y	S	G	F	S	S	P	R	V	E	W	K	F	V	Q	G	S	T	T	A	L	V	C	Y	N	S	Q	I	T	A	P	Y	A	D	R	V	T	F	S	S	S	G	I	T	F	S	S	V	T
40628	51	A	Y	S	G	F	S	S	P	R	V	E	W	K	F	D	Q	G	D	T	T	R	L	V	C	Y	N	N	K	I	T	A	S	Y	E	D	R	V	T	F	L	P	T	G	I	T	F	K	S	V	T
jam	100	R	K	D	N	G	E	Y	T	C	M	V	S	E	E	G	G	Q	N	Y	G	E	V	S	I	H	L	T	V	L	V	P	P	S	K	P	T	I	S	V	P	S	S	V	T	I	G	N	R	A	V
40628	101	R	E	D	T	G	T	Y	T	C	M	V	S	E	E	G	G	N	S	Y	G	E	V	K	V	K	L	I	V	L	V	P	P	S	K	P	T	V	N	I	P	S	S	A	T	I	G	N	R	A	V
jam	150	L	T	C	S	E	H	D	G	S	P	P	S	E	Y	S	W	F	K	D	G	I	S	M	L	T	A	D	A	K	K	T	R	A	F	M	N	S	S	F	T	I	D	P	K	S	G	D	L	I	F
40628	151	L	T	C	S	E	Q	D	G	S	P	P	S	E	Y	T	W	F	K	D	G	I	-	V	M	P	T	N	P	K	S	T	R	A	F	S	N	S	S	Y	V	L	N	P	T	T	G	E	L	V	F
jam	200	D	P	V	T	A	F	D	S	G	E	Y	Y	C	Q	A	Q	N	G	Y	G	T	A	M	R	S	E	A	A	H	M	D	A	V	E	L	N	V	G	G	I	V	A	A	V	L	V	T	L	I	L
40628	200	D	P	L	S	A	S	D	T	G	E	Y	S	C	E	A	R	N	G	Y	G	T	P	M	T	S	N	A	V	R	M	E	A	V	E	R	N	V	G	V	I	V	A	A	V	L	V	T	L	I	L
jam	250	L	G	I	L	I	F	G	V	W	F	A	S	R	G	Y	F	E	T	T	K	K	G	T	A	P	G	K	K	V	I	Y	S	O	P	S	T	R	S	E	G	E	F	K	O	T	S	S	F	L	
40628	250	L	G	I	L	V	F	G	I	W	F	A	S	R	G	H	F	D	R	T	K	K	G	T	-	S	S	K	K	V	I	Y	S	O	P	S	A	R	S	E	G	E	F	K	O	T	S	S	F	L	
jam	300	V																																																	
40628	299	V																																																	

Figure 15

Figure 15

SEQ ID NO:10 jam 1 M G T E G K A G R K L L F L F T S M I L G S L V Q G K G S V Y T A O S D V O V P E N E S I K L T
 SEQ ID NO:2 45416 1 - - - - - M G I L L G L L L L G H L T V D T Y G R P I L E V P E S V T G P W K G D V N L P

jam 49 C T Y S - - - G F S S P R V E W K F V O G S T T A L V - - - C Y N S O I T A P Y A D R V T F S -
 45416 41 C T Y D P L Q G Y T Q V L V K W L V O R G S D P V T I F L R D S S G D H I Q O A K Y O G R L H V S H

jam 90 - - - S S G I T F S S V T R K D N G E Y T C M V - - - S E E G G O N Y G E V S I H L T V L - V P P
 45416 91 K V P G D V S L O L S T L E M D D R S H Y T C E V T W O T P D G N O V V R D K I T E L R V O K L S V

jam 132 S K P T I S V P S - - - S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A
 45416 141 S K P T V T T G S G Y G F T Y P O G M R I S L O C Q A R G S P P I S Y I W Y K O O T N - - N O E P

jam 178 K T R A F M N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C O A O N G Y G T A M R S E A A
 45416 188 I K V A T L - - - - - S T L L F K P A V I A D S G S Y F C T A K G O V G S E Q H S D I V

jam 228 H - - - M D A V E L N V G G I V A A V L V T L I L L G L L I F G - - - V W F A Y S R G Y F E T T K K
 45416 227 K F V V K D S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W D W T T D M D G Y L G E T S A

jam 272 G T A P G K K V I Y S O P S T R S E G E F K O T S S F L V
 45416 277 G P G K S L P V F A I I L I I S L C C M V V F T M A Y I M L C R K T S O Q E H V Y E A A R

Figure 16

SEQ ID NO:10 jam 1 MGTEGKAGRKLFLFTSMILGSLVOGKGSVYTAQSDVQV - - PENESIKL
SEQ ID NO:29 35638 1 - - MARRSRHRLLLLLRLVVALGYHKAYGFSAPKDQQVVTAVEYOEAIL

jam 48 TC - TYSGFSSPRVEWKFVOGSTTALVCYNSQITAPYADRVTFSSSGITFS
35638 49 ACKTPKKTVS SRL EWKXL - GRSVSFVY YQOTLQGDFKNRAEMIDFNIRIK

jam 97 SVTRKDNGEYTCMVS - - EEGGONYGEVSIHLTVLVPPSKPTISVPSSVTI
35638 98 NVT.RSDAGKYRCEVSA PSEOGQNL EEDTVTL EVLVAPAVPSCEVPSSALS

jam 145 GNRAVLTCSEHDGSPPS EYSWFKDGISMLTADAKKTRAFMNSSFTIDPKS
35638 148 GTVVELRCODKEGNPAPEYTWFKDGI RLL - ENPRLGSOSTNSSYTMNTKT

jam 195 GD LIFOPVTA FDSGEYYCOAONGYGTAMRSEAAHMDAVE LNVGGIVAAVL
35638 197 GTLOFNTVSKLDTGEYSCEARN SVG - YRRCPGKRMOVDDL NISGIIAAVV

jam 245 VTLLLLGLLIFGVWFAYSR GYFETTKKGTA PGKKVIYSOPSTRSEGEFKO
35638 246 VVALVISVCGLGVCYAORKGYF - - SKETSFOKSNSSSKATTMSENVOWL

jam 295 TSSFLV
35638 293 TPVIPALWKAAAGGSRGOEF

Figure 17

SEQ ID NO:6 A33_hum

SEQ ID NO:10 jam

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Figure 18

cDNA hybridization of A33 homolog 40628 to human tissues

<u>Tissue</u>	<u>Expression</u>
whole brain	+
amygdala	+
caudate nucleus	+
cerebellum	-
cerebral cortex	+
frontal lobe	+
hippocampus	+
medulla oblongata	+
occipital lobe	+
putamen	+
substantia nigra	+
temporal lobe	+
thalamus	+
nucleus accumbens	+
spinal cord	-
heart	++
aorta	+
skeletal muscle	+
colon	+++
bladder	++
uterus	+
prostate	+++
stomach	+++
testis	++
ovary	+++
pancreas	++
pituitary gland	++
adrenal gland	++
thyroid gland	++
salivary gland	+++
mammary gland	++
kidney	+++
liver	++
small intestine	++
spleen	++
thymus	++
peripheral leukocyte	+
lymph node	+
bone marrow	+
appendix	+
lung	++++
trachea	++++
placenta	++++
fetal brain	+
fetal heart	+
fetal kidney	++
fetal liver	+++
fetal spleen	+
fetal lung	++++

Figure 19

Elevated mRNA for Murine JAM in CRF2-4 -/- Colitic Mice as Compared to Wildtype Mice

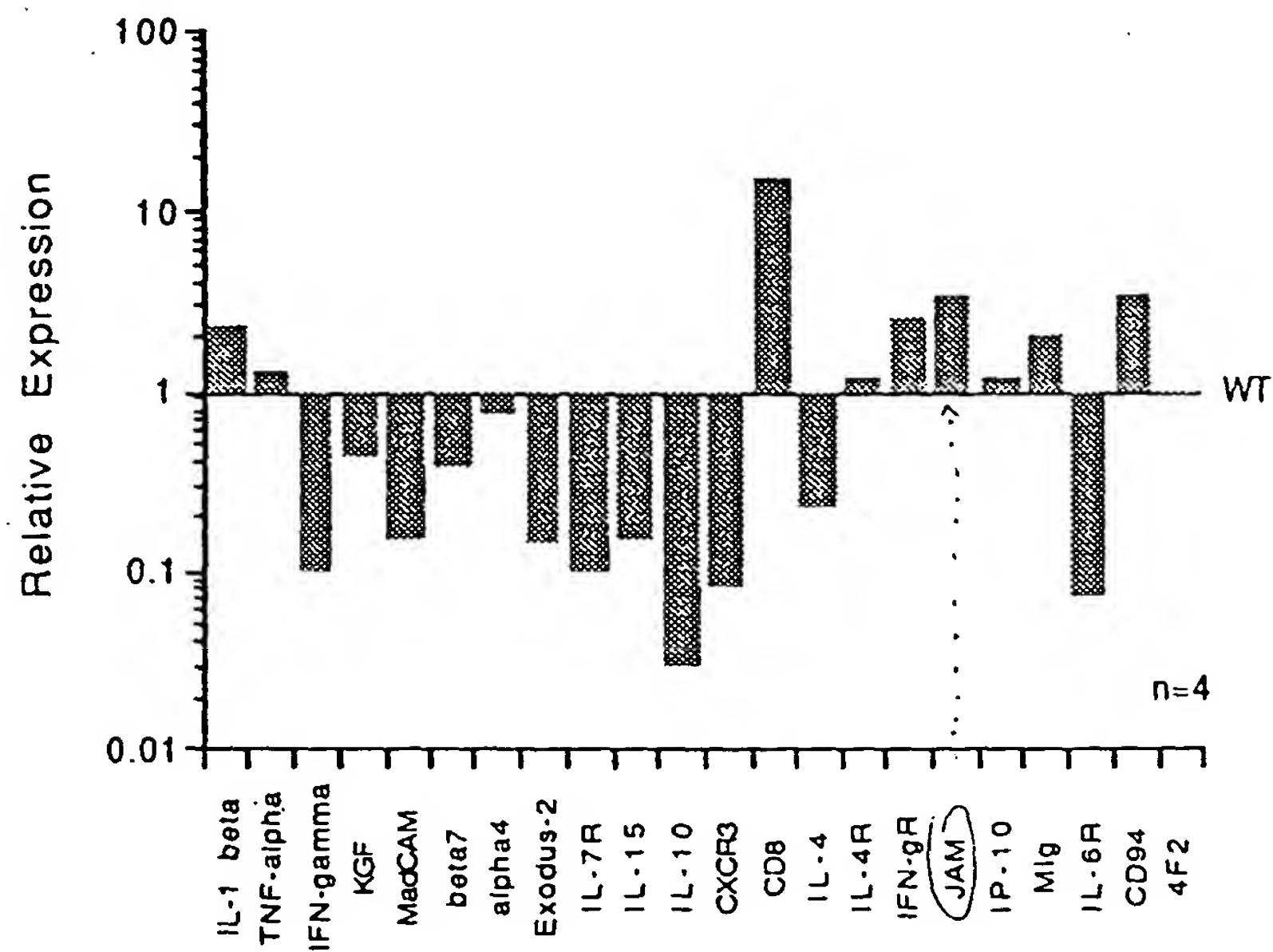


Figure 20

PIN370 Binds to the Cell Surface of Human Neutrophils

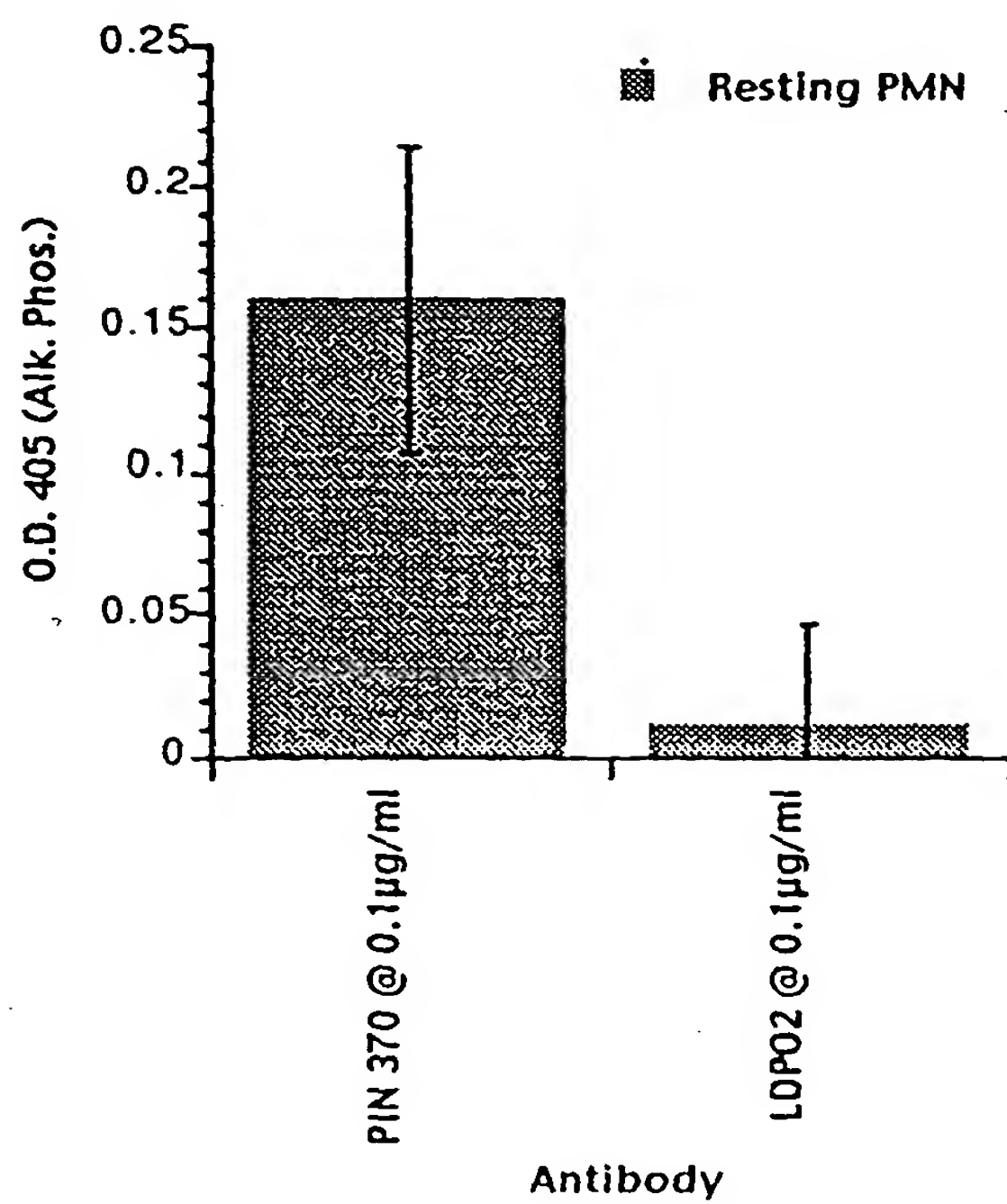


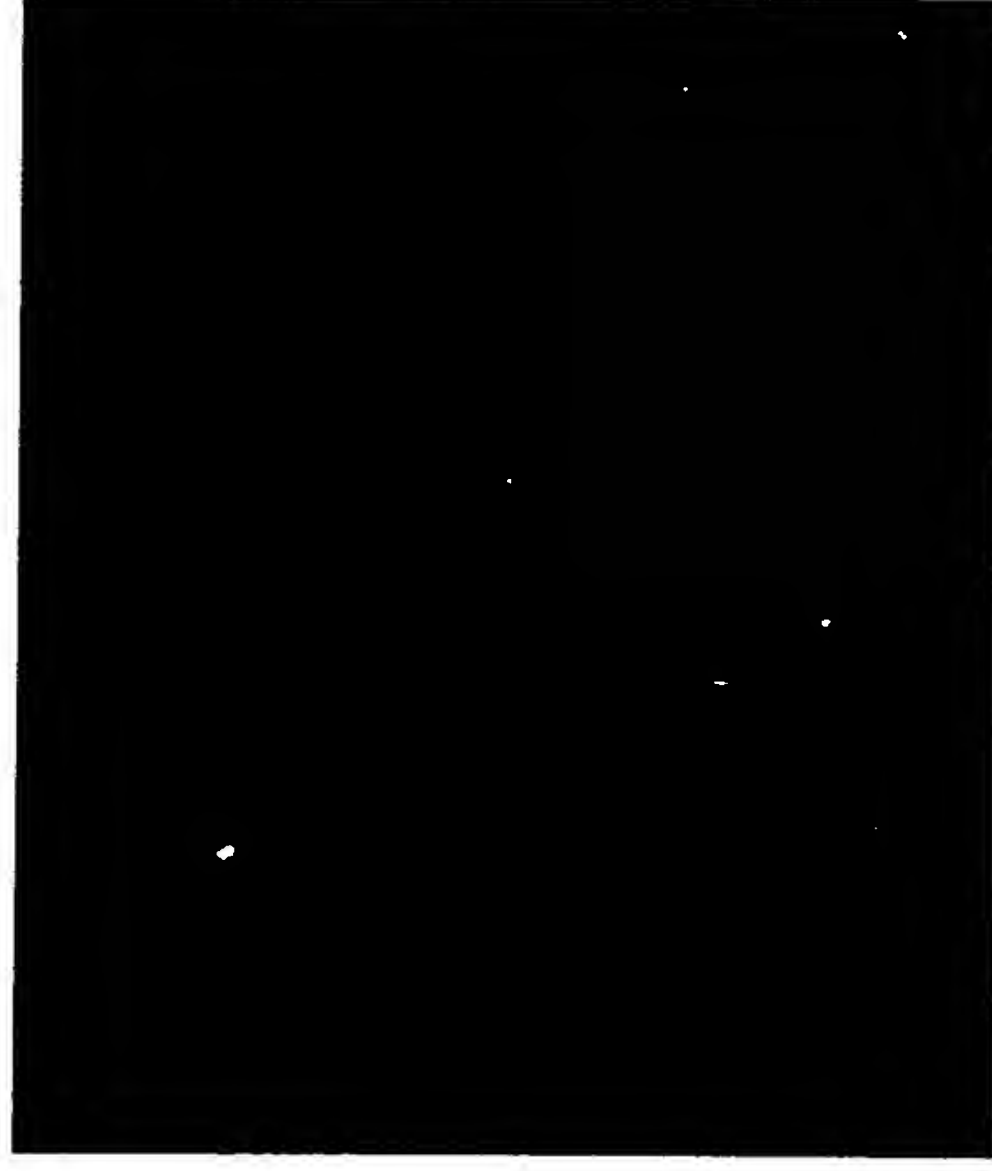
Figure 21

Figure 22

1 MALRRPPRLRICARLPDEFLLFRGCLIGAVNLKSSNRTFVVQEFESVELSCIITDSQT
61 SDPRIEWKKIQDEQTTYVFEDNKIQGDLAGRAEILGKTSLKIVVNVTRRDSALYRCWAR
121 NDRKEIDEIVIELTVQVKPVT PVC RV PKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL
181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIA S NDAGSARCEEQEMEYVDL
241 NIGGI GGVLVLA V L A L I T L G I C C A Y R R G Y F I N N K Q D G E S Y K N P G K P D G V N Y I R T D E E G
301 DFRHKSSEVI

Figure 23

IgG Control



20x

6F.1 (anti-Pro362 STIgMA)



10x
6F.1 (anti-Pro362)

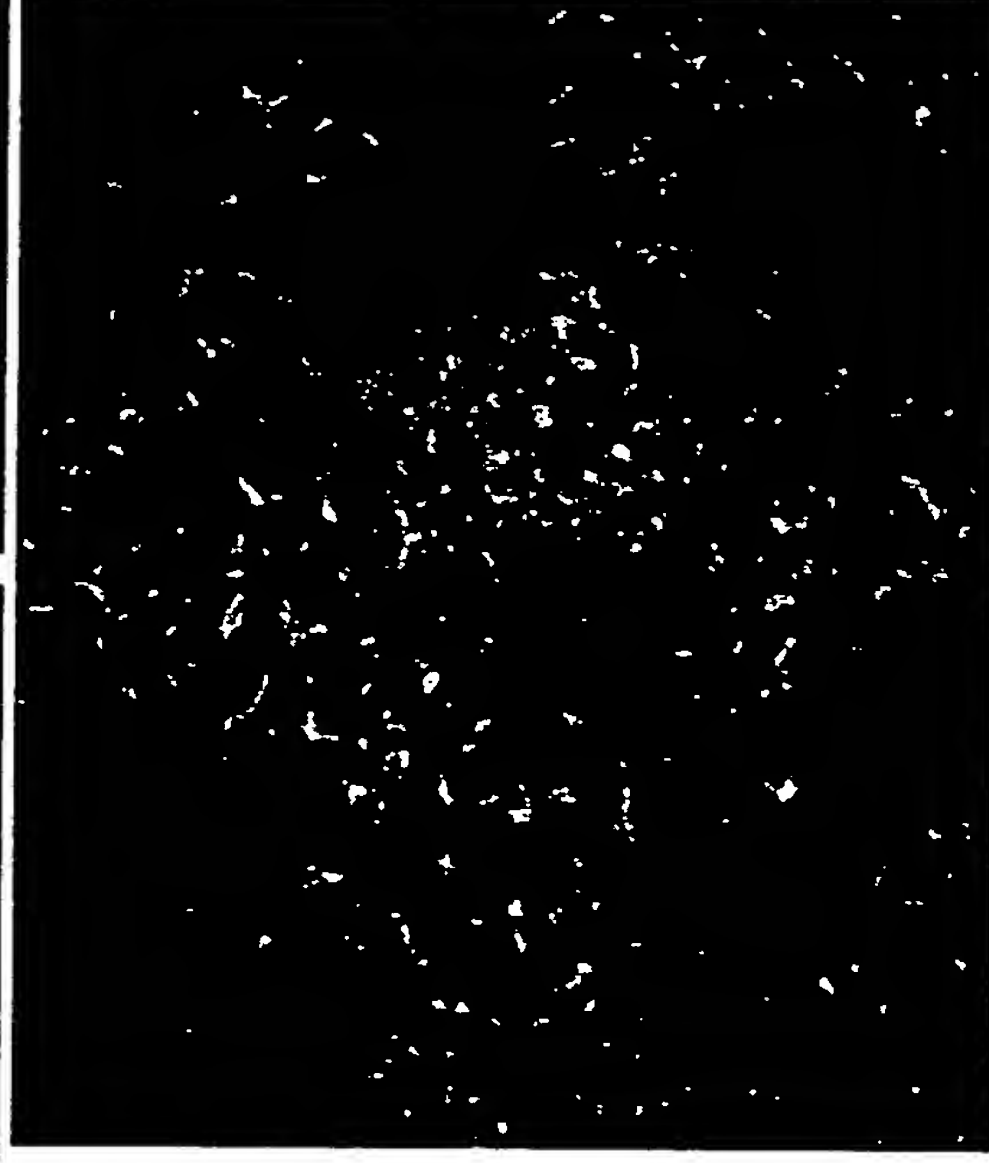


Figure 24

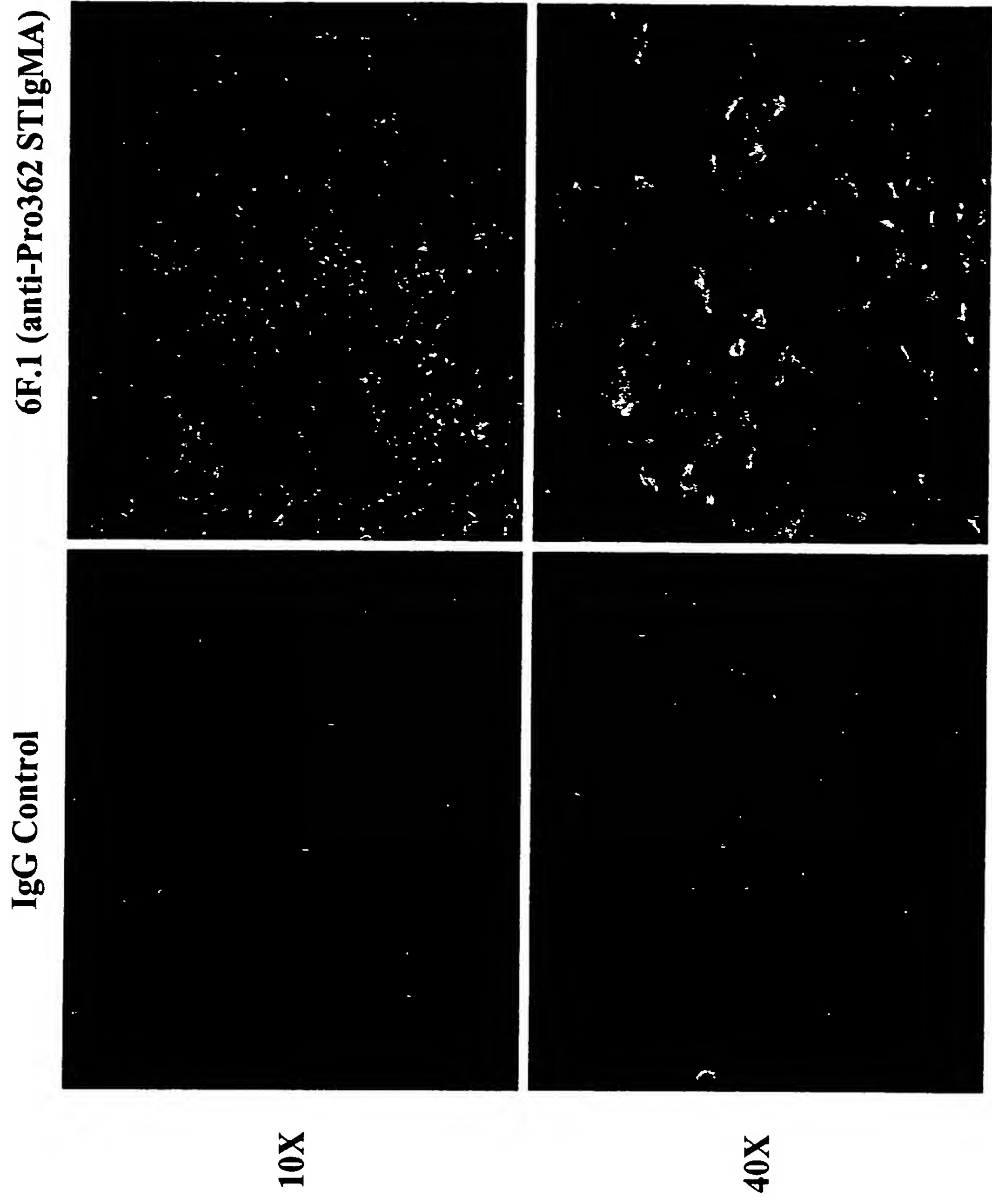
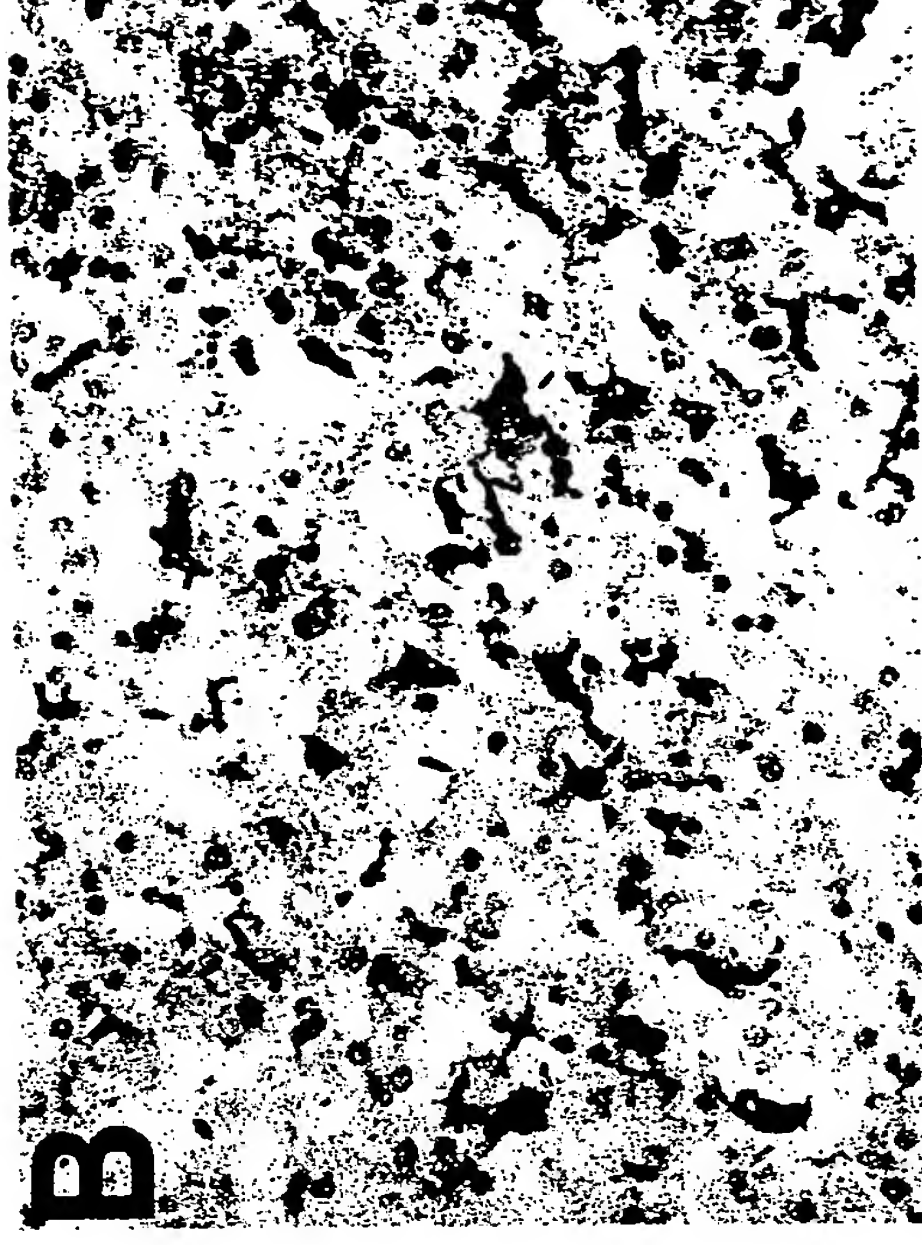


Figure 25

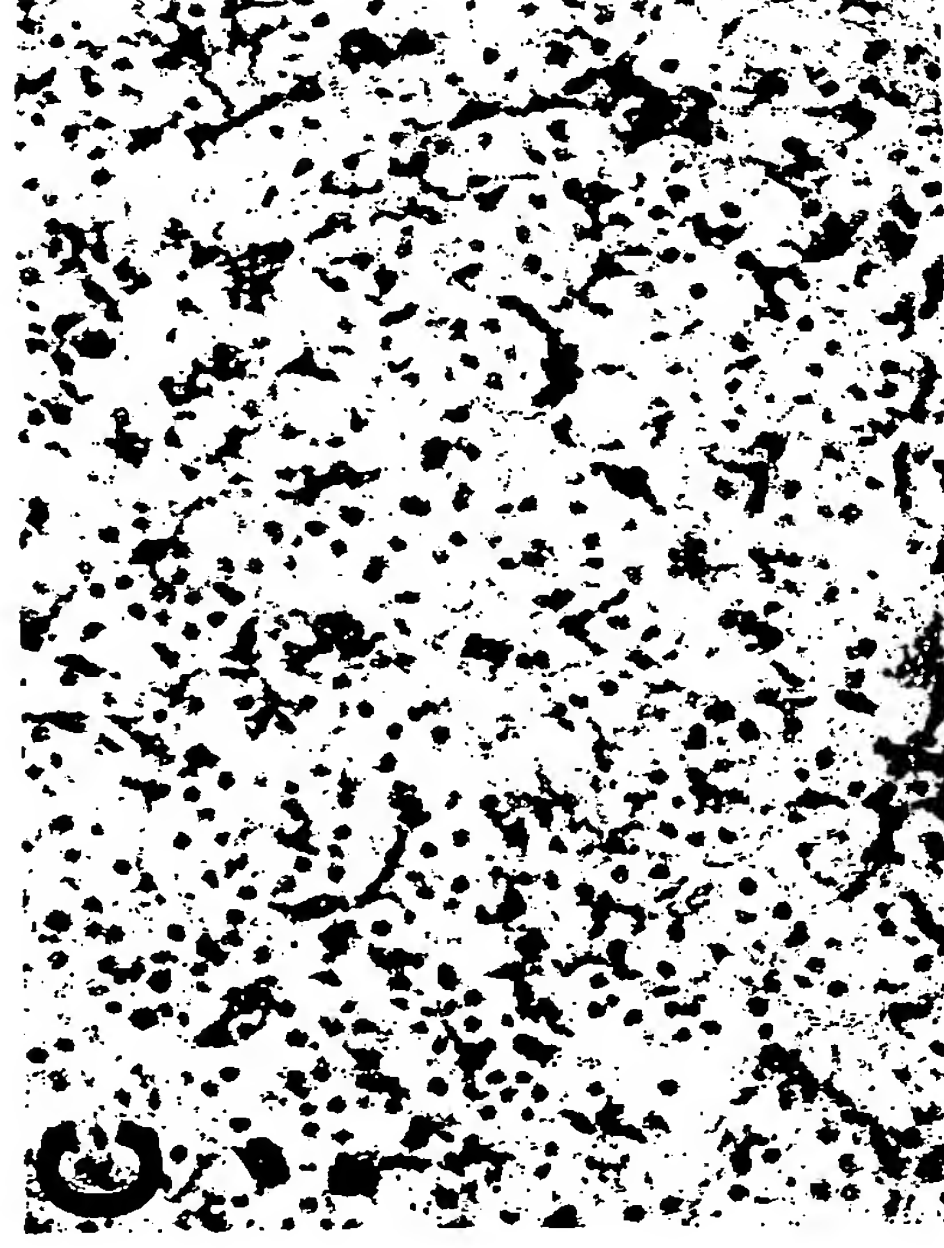
Colon Macs



Kupffer cells



Adrenal Macs



Hofbauer cells



Figure 26

Synovial cells



Figure 27

RA Synovium

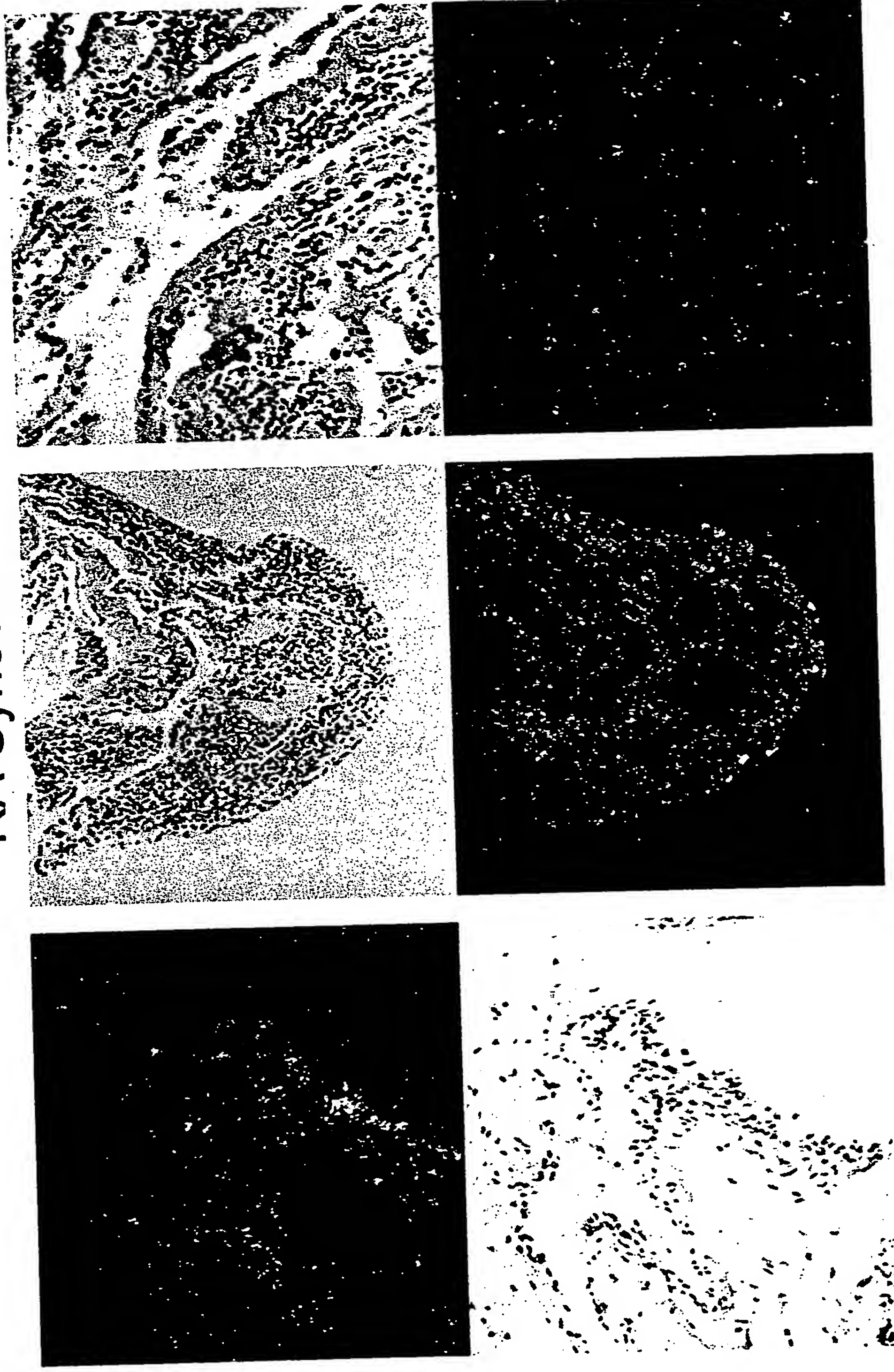


Figure 28

Brain Microglia

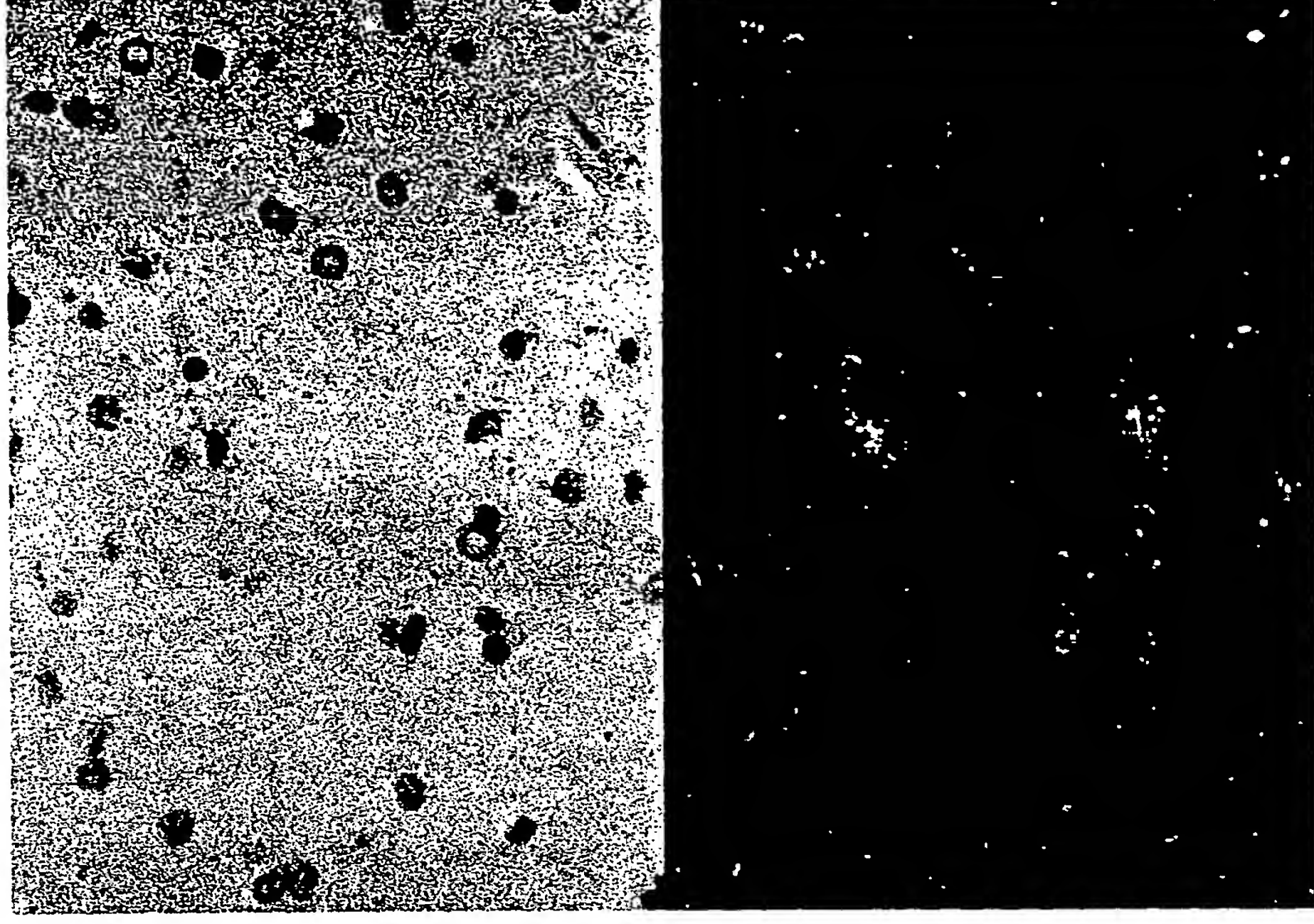
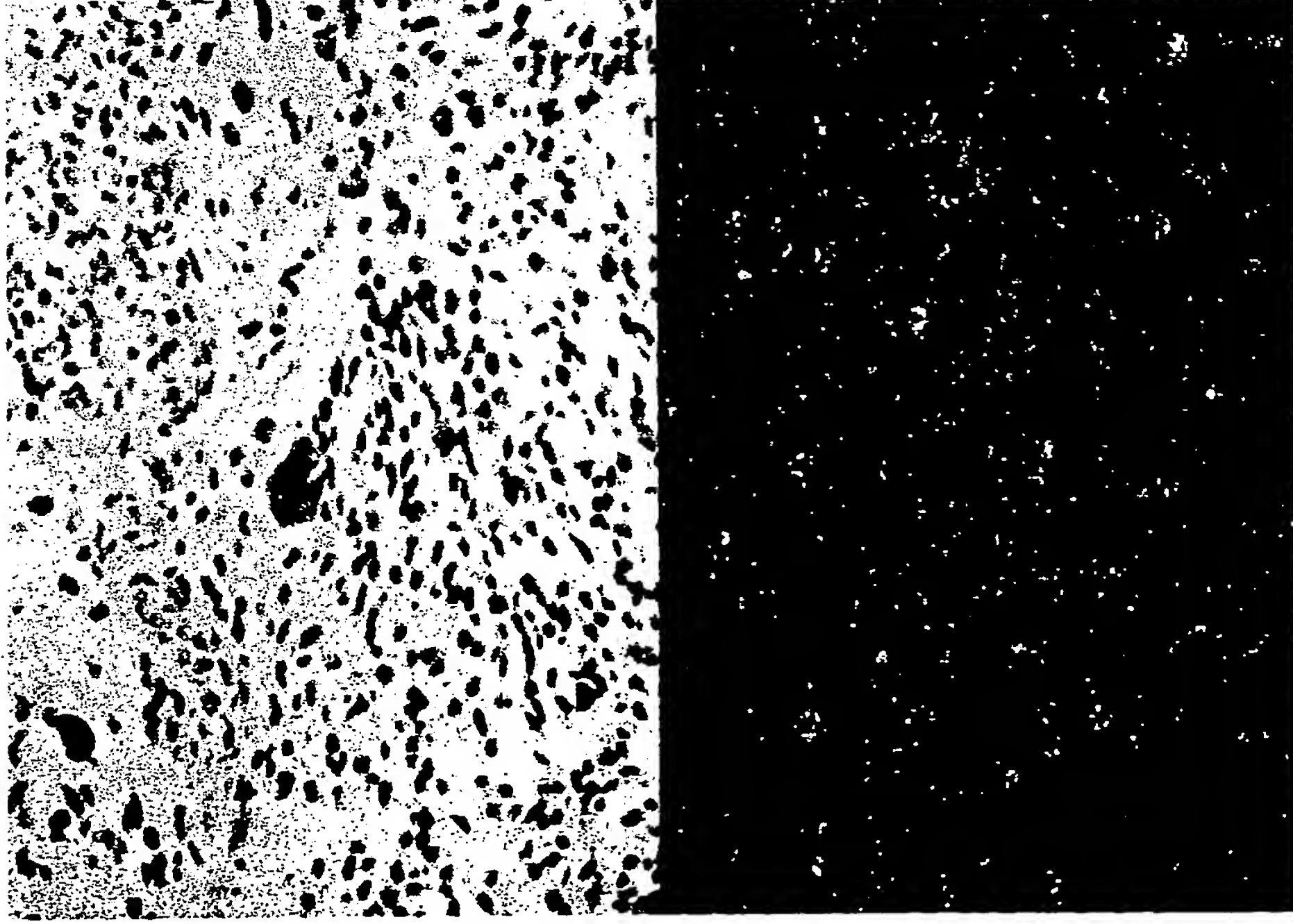


Figure 29

Alveolar Macs

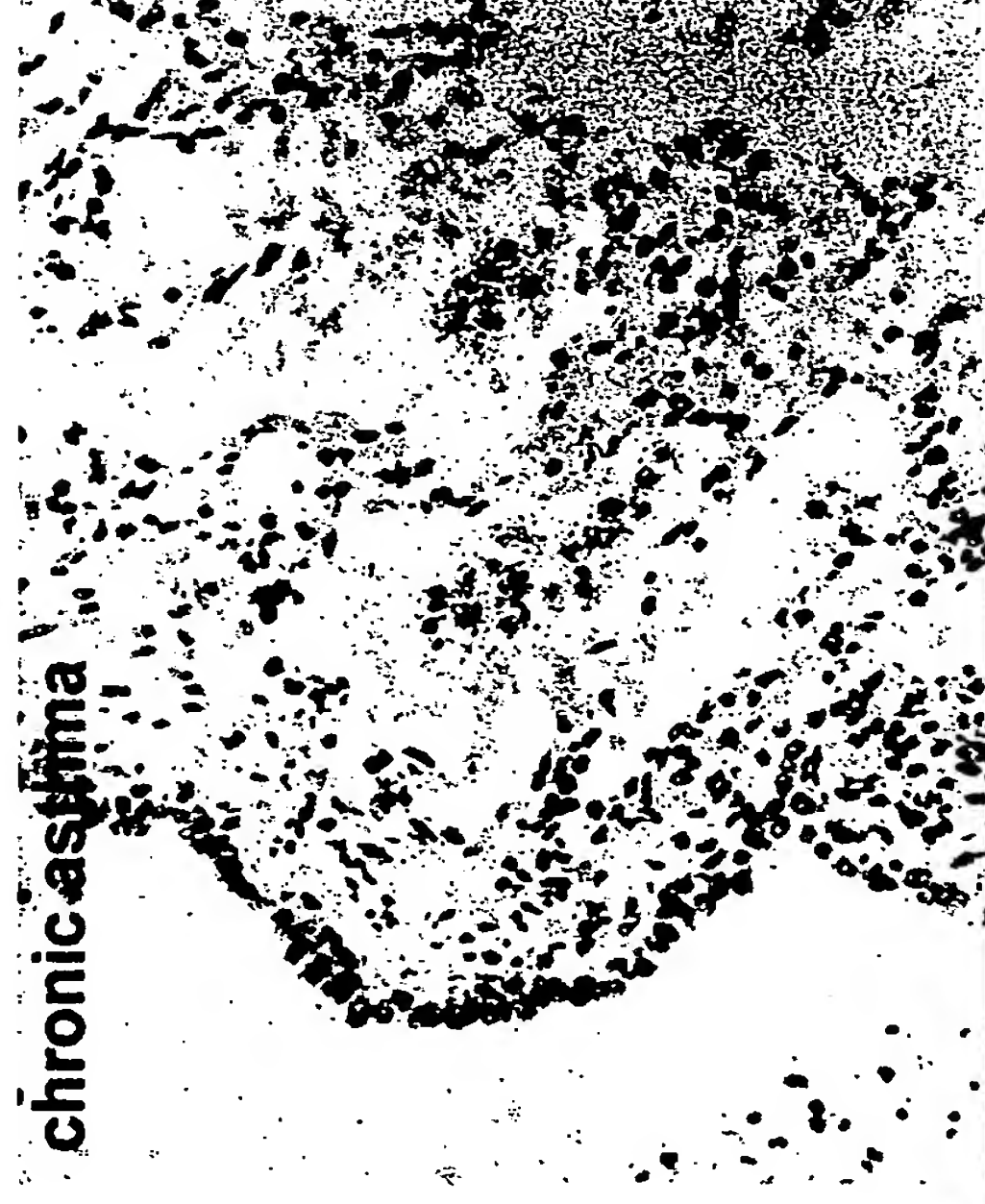


Figure 30

Liver Kupffer cells

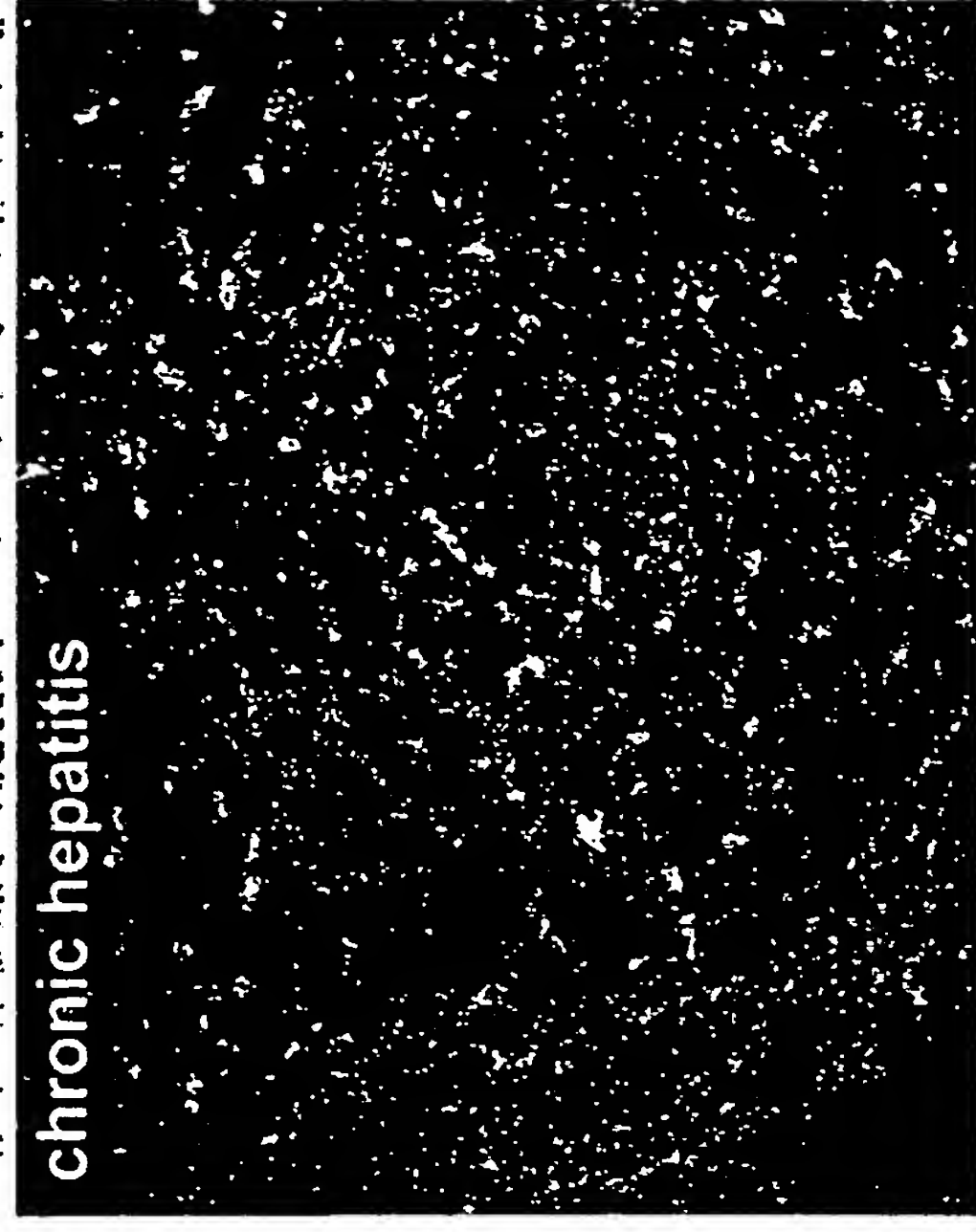
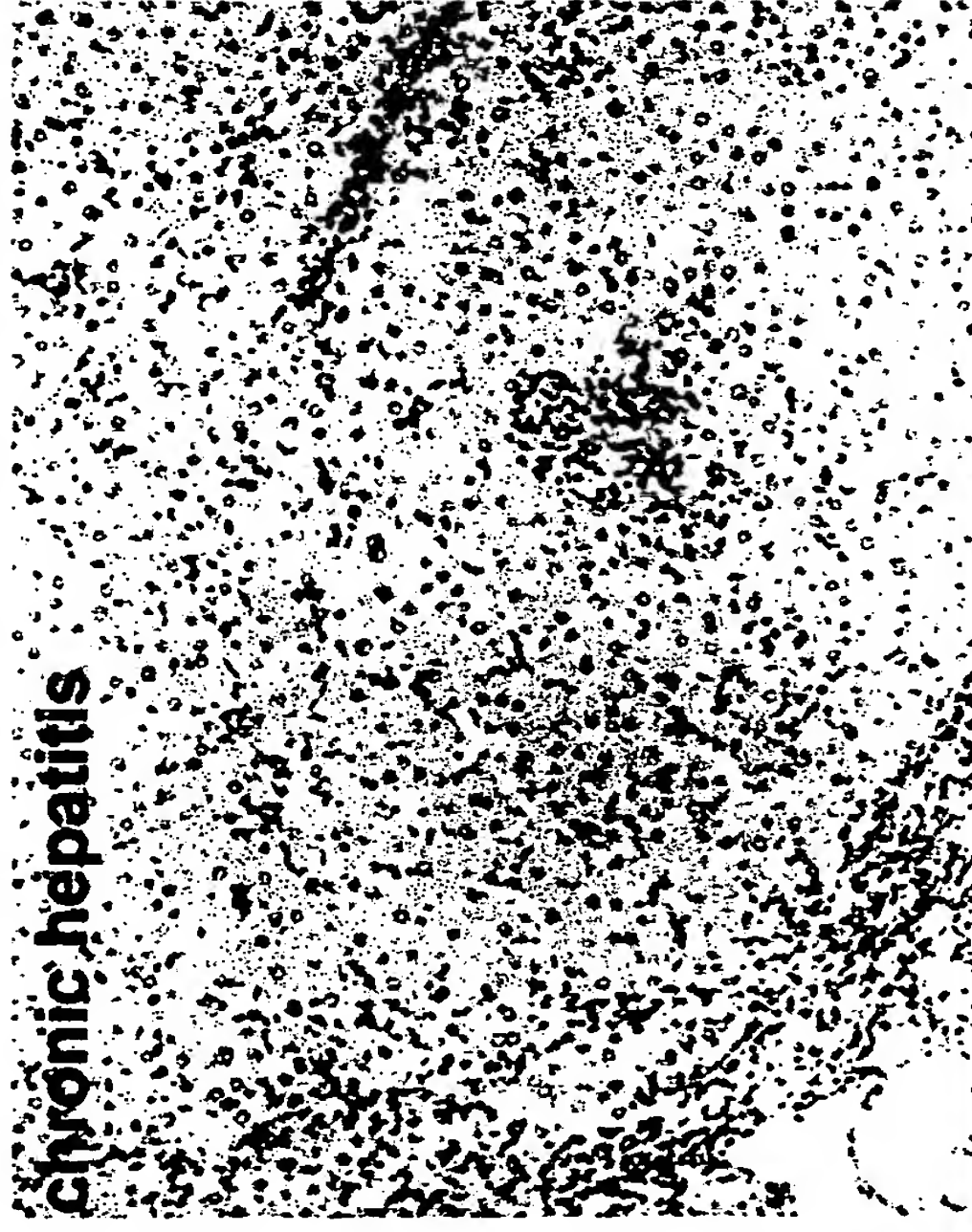


Figure 31

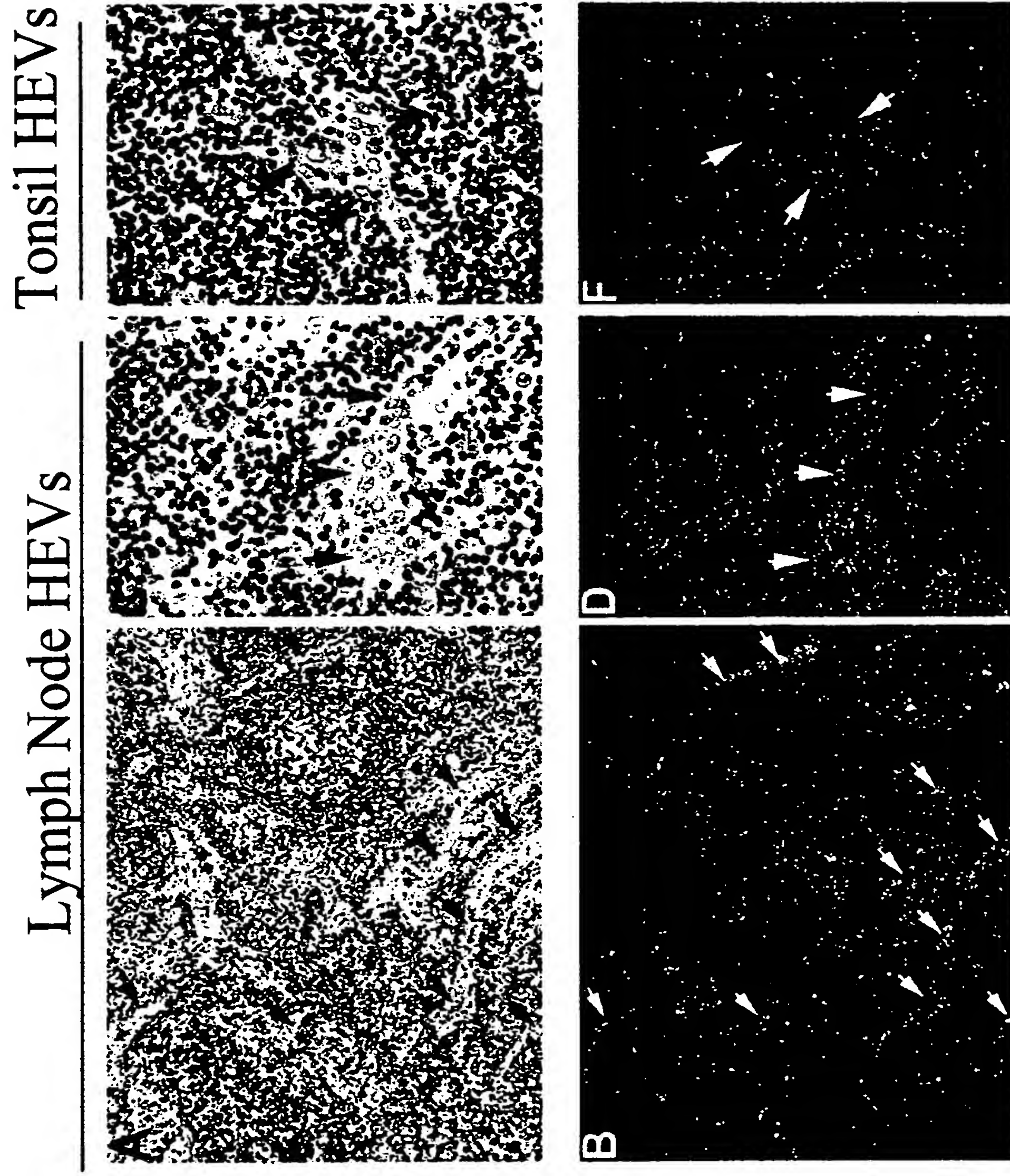


Figure 32

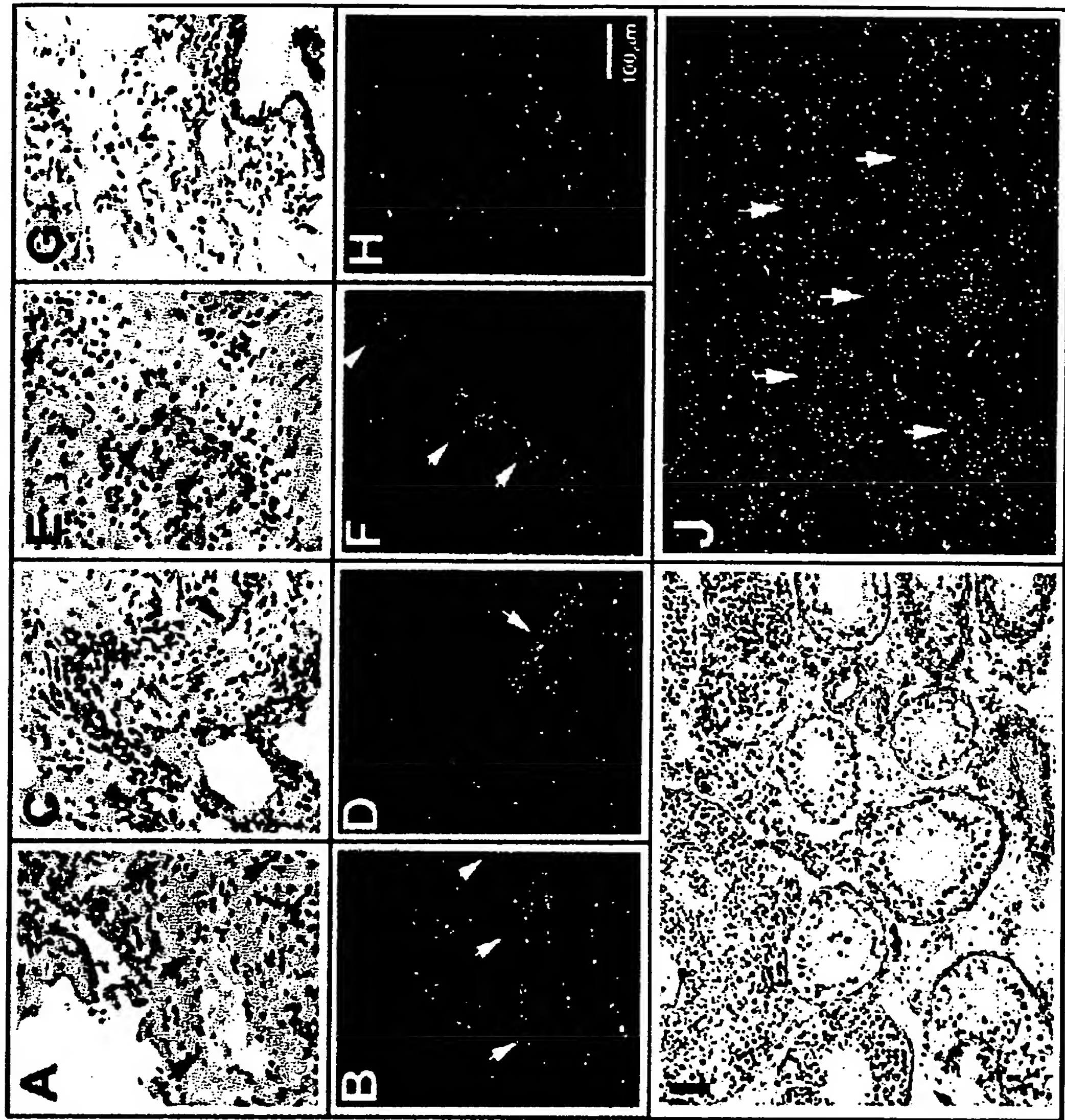


Figure 33

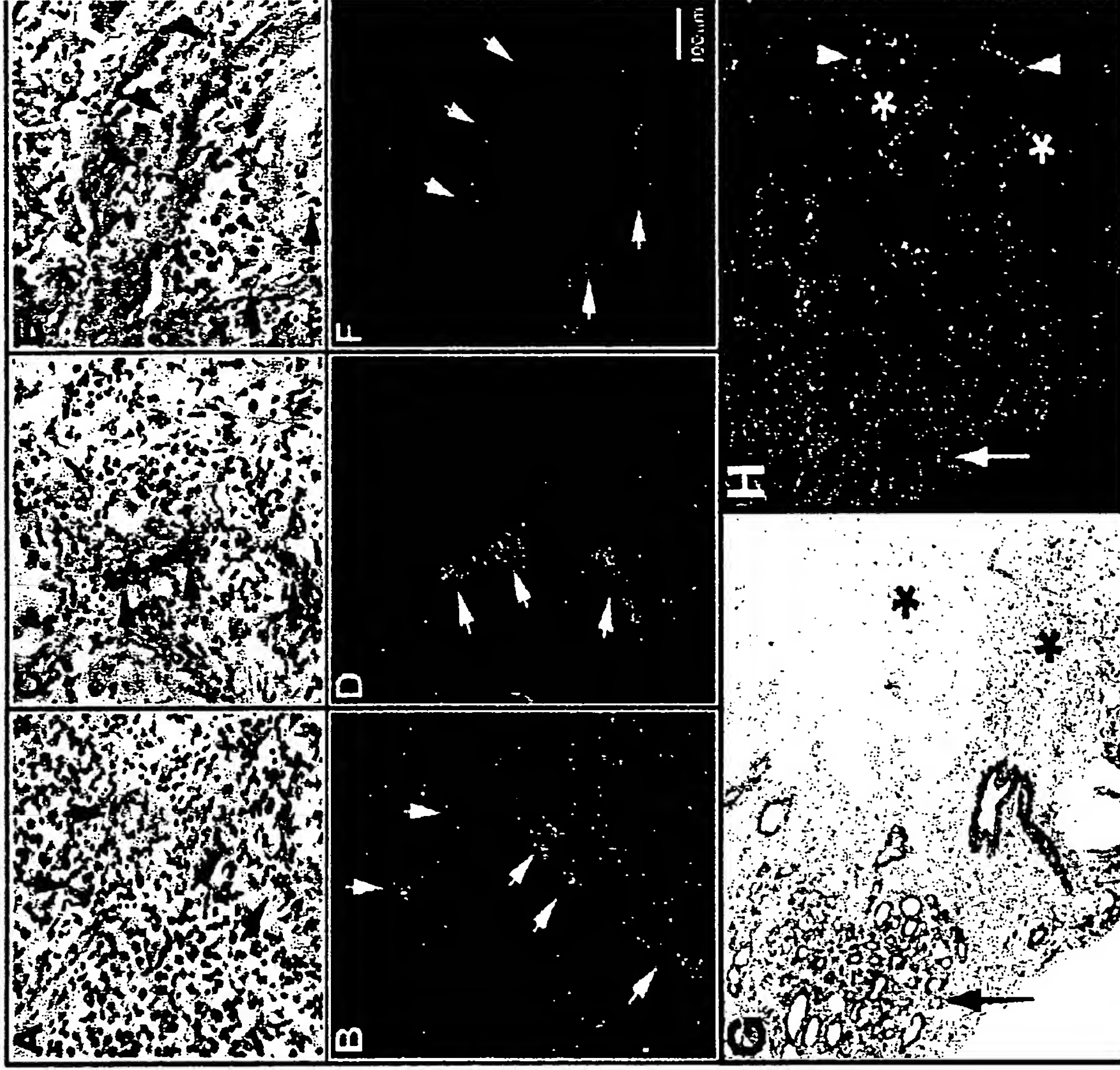


Figure 34

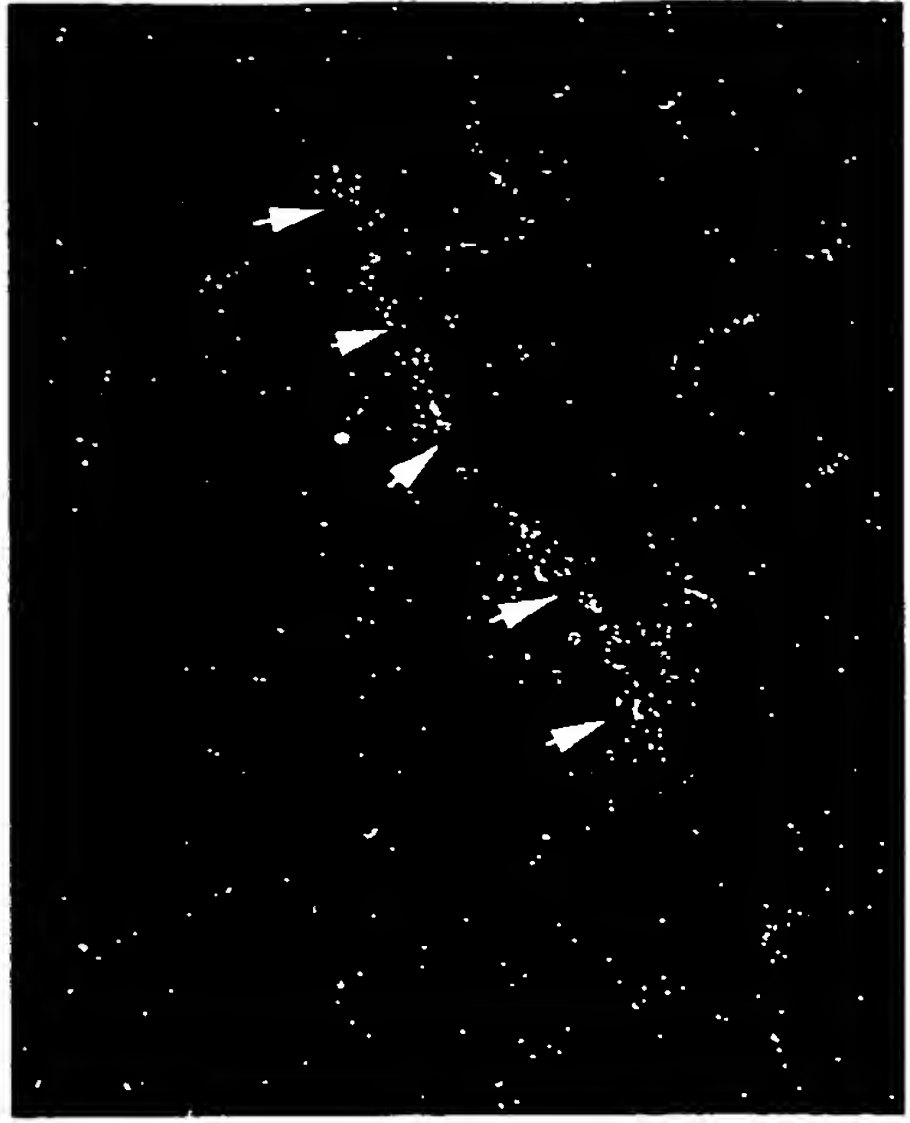
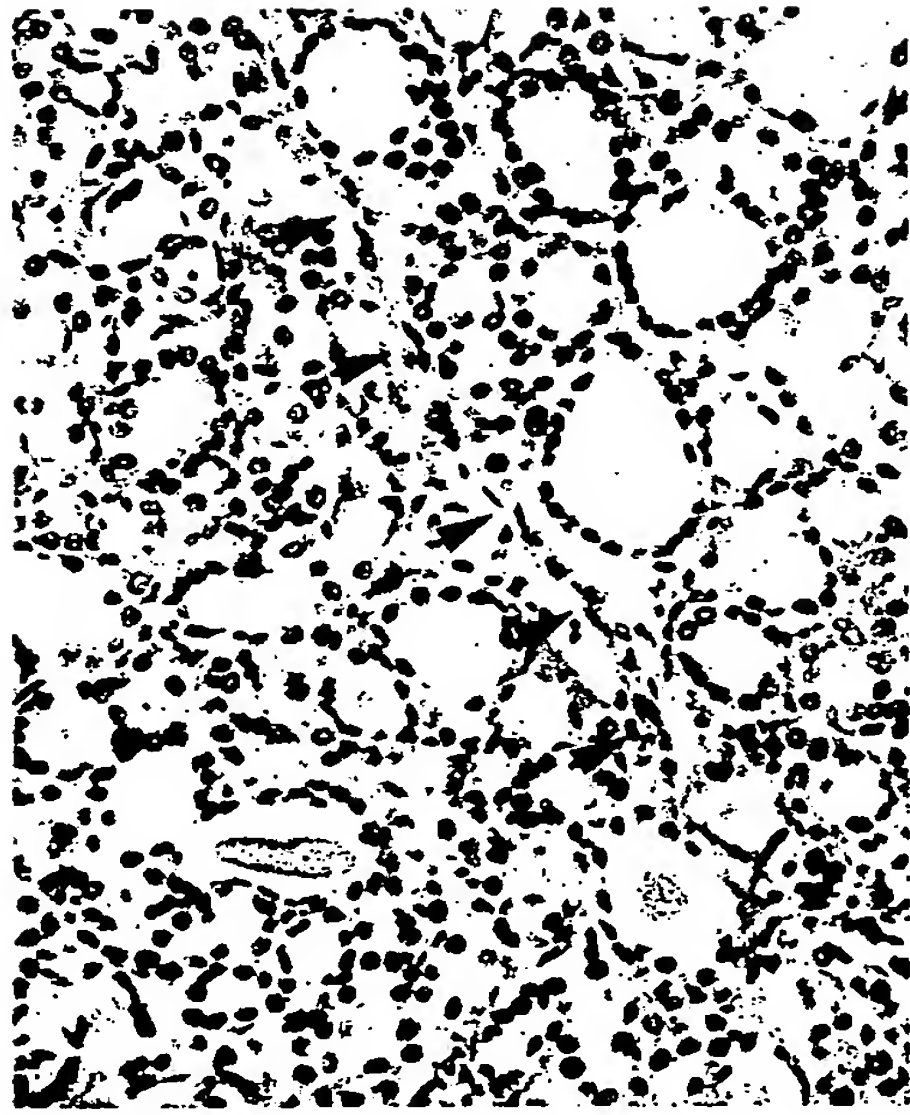


Figure 35

DUAL STIgMA-CD68 IHC

Adrenal gland macrophages



Adrenal-STIgMA



Adrenal-CD68



Adrenal-STIgMA/CD68

Figure 36

Liver Kupffer cells



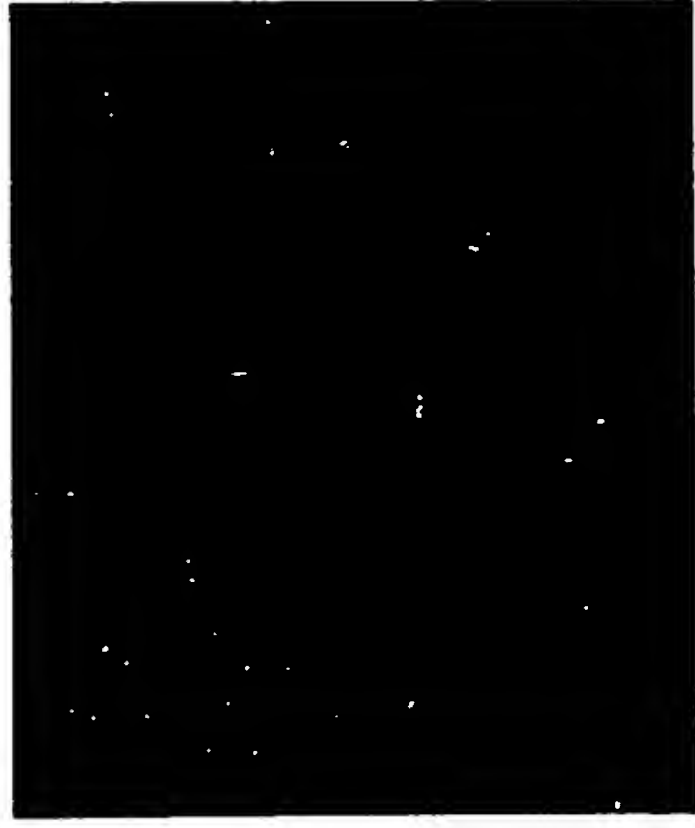
Liver-STIgMA



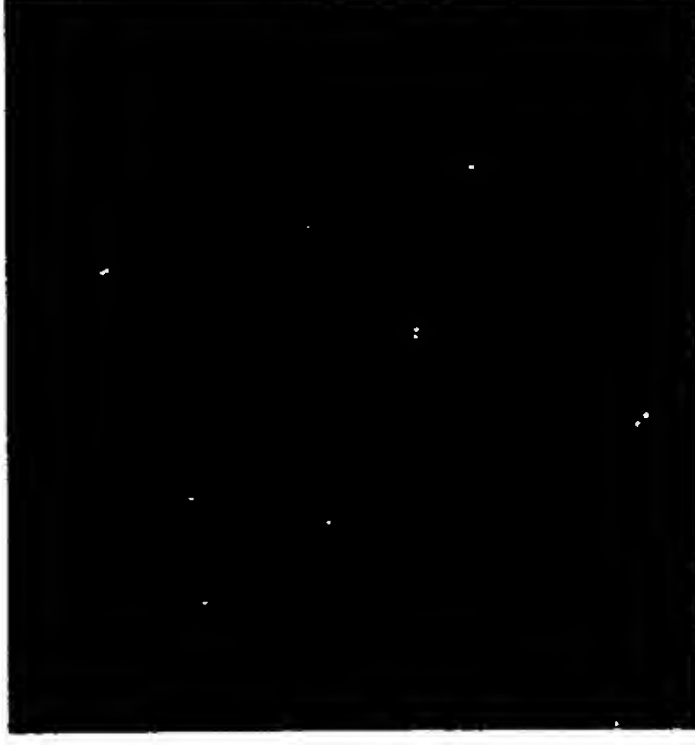
Liver-CD68

Figure 37

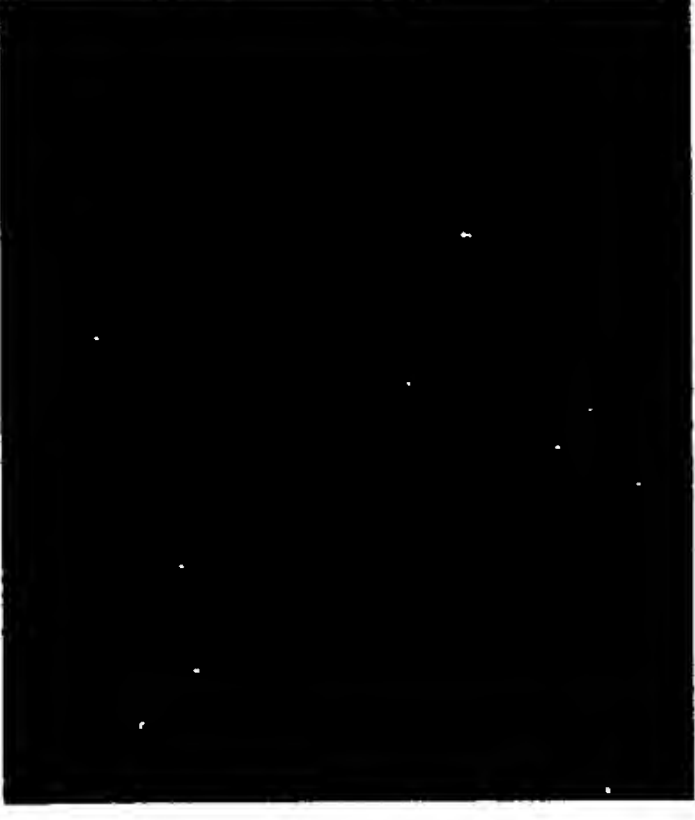
Brain Microglial cells



Brain-STIgMA



Brain-CD68



Brain-STIgMA/CD68

Figure 38

Placental Hofbauer cells



Placenta-STIgMA



Placenta-CD68



Placenta-STIgMA/CD68

Figure 40

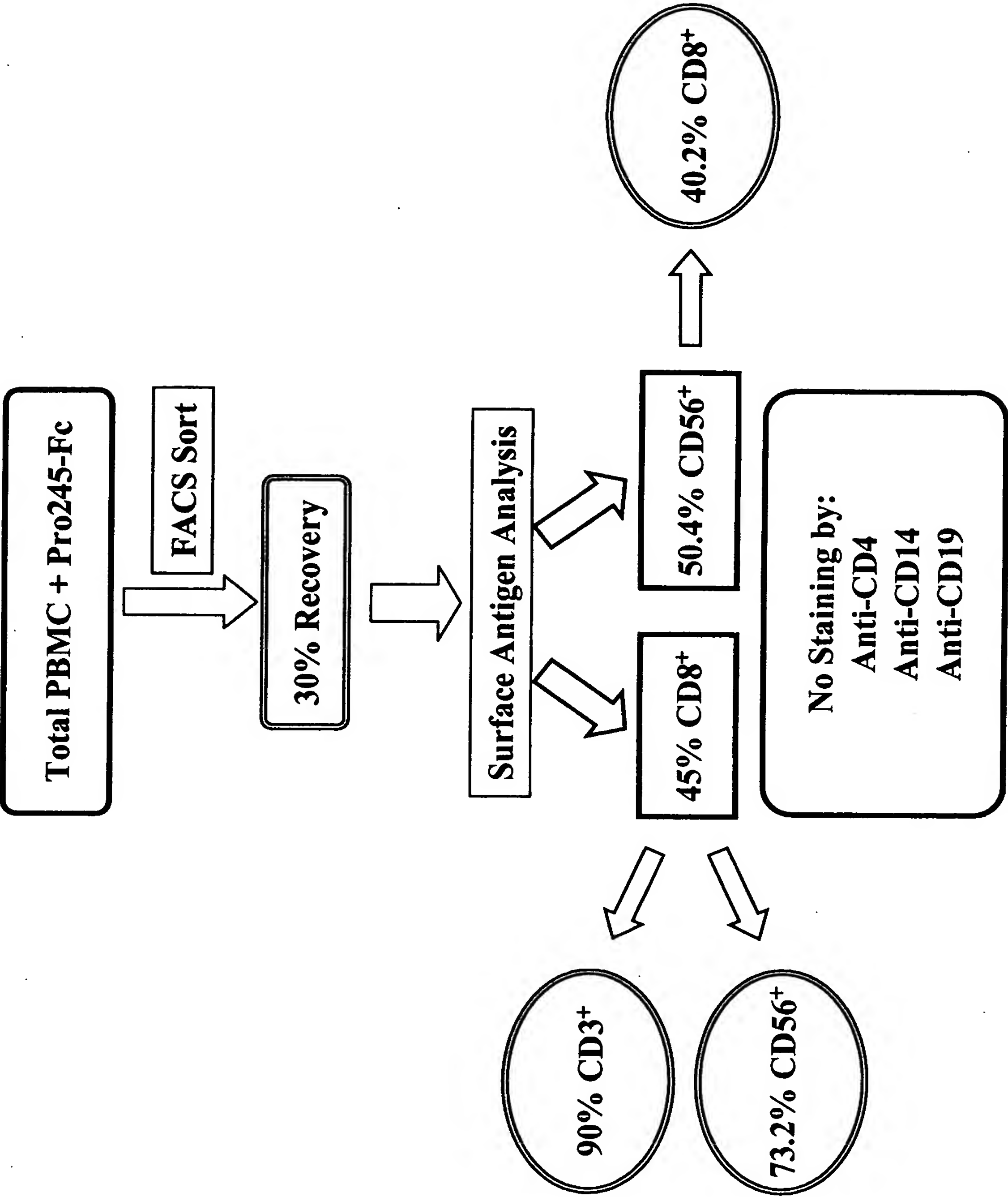


Figure 41

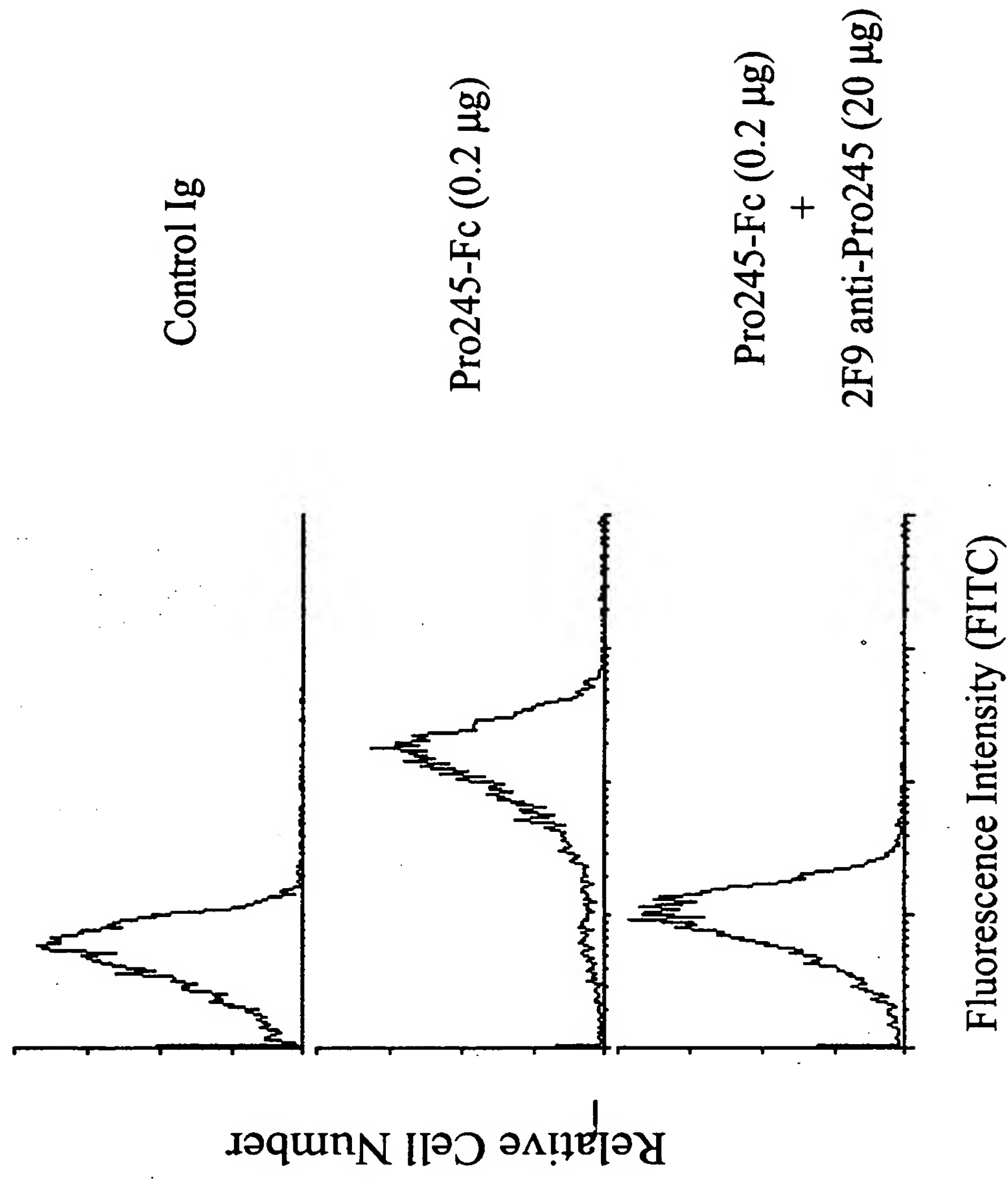


Figure 42

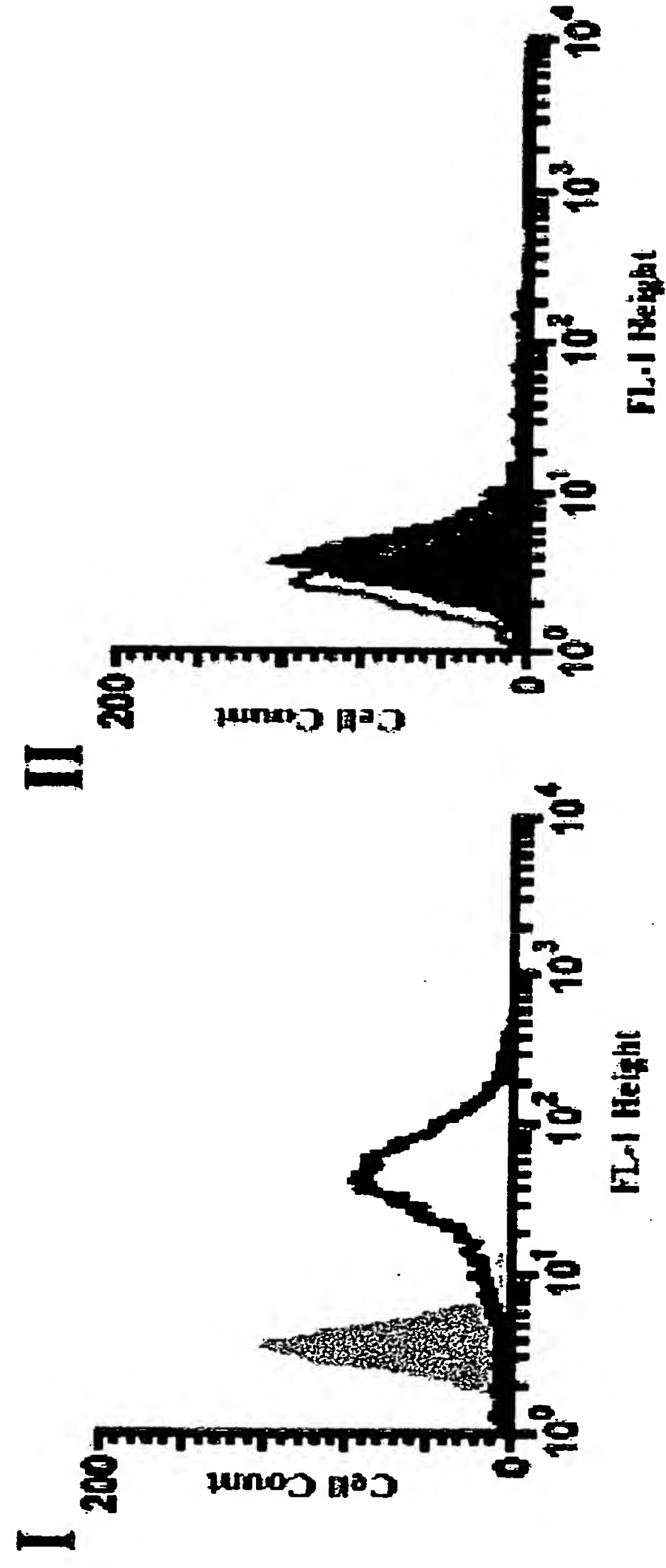


Figure 43

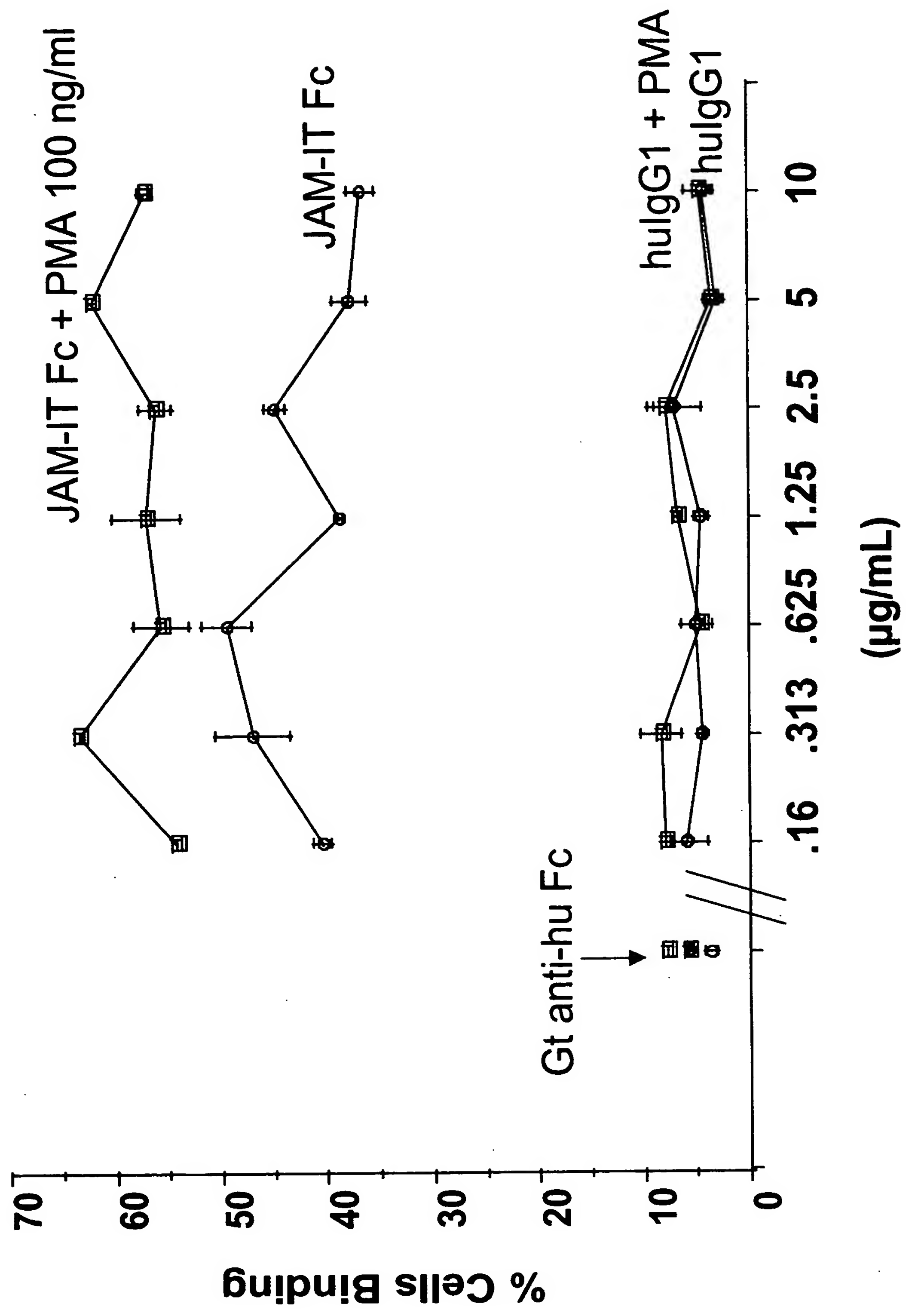


Figure 44

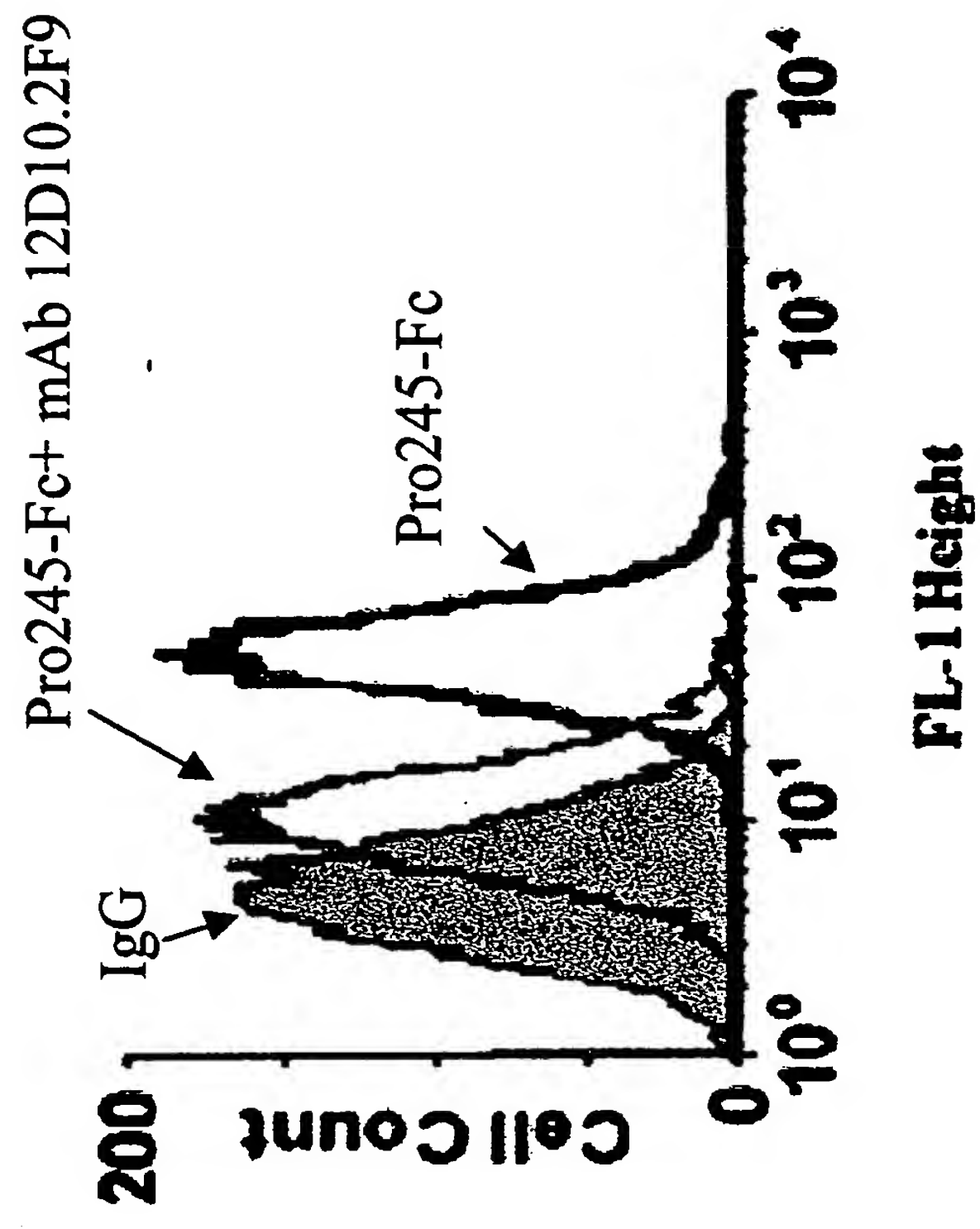


Figure 45

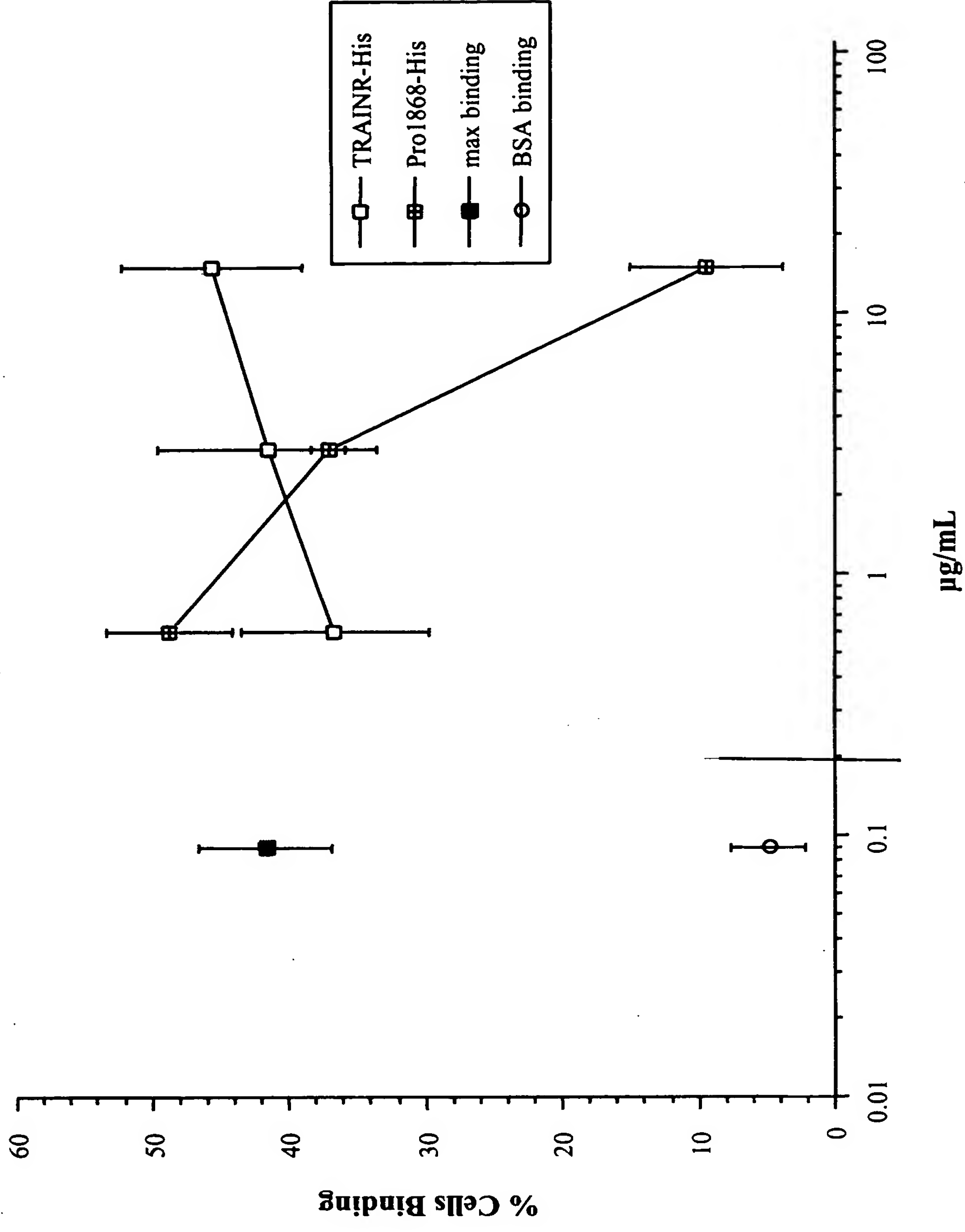
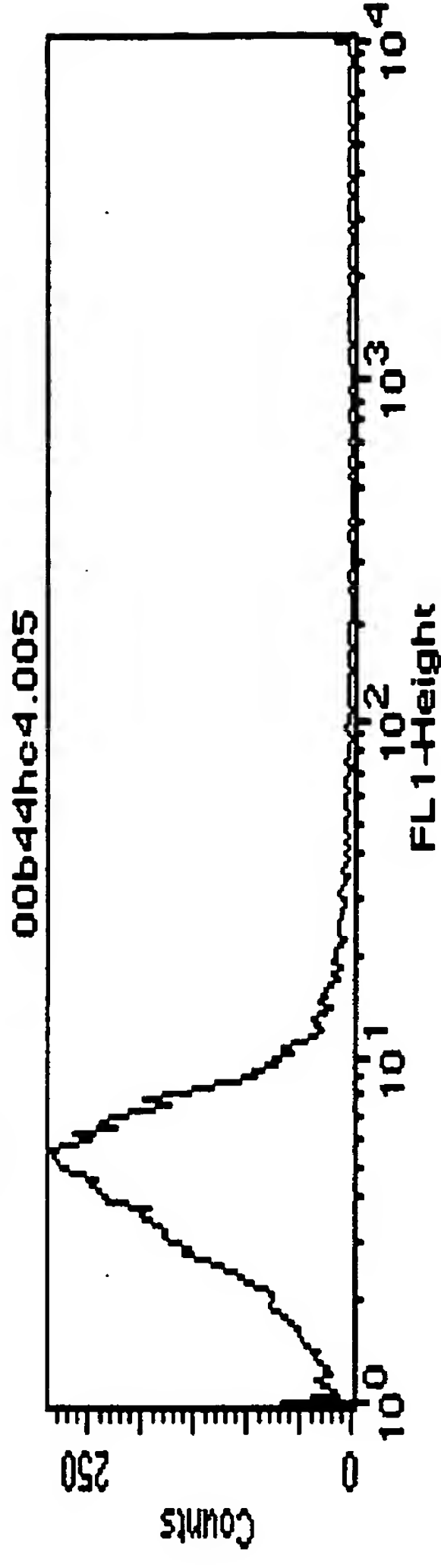
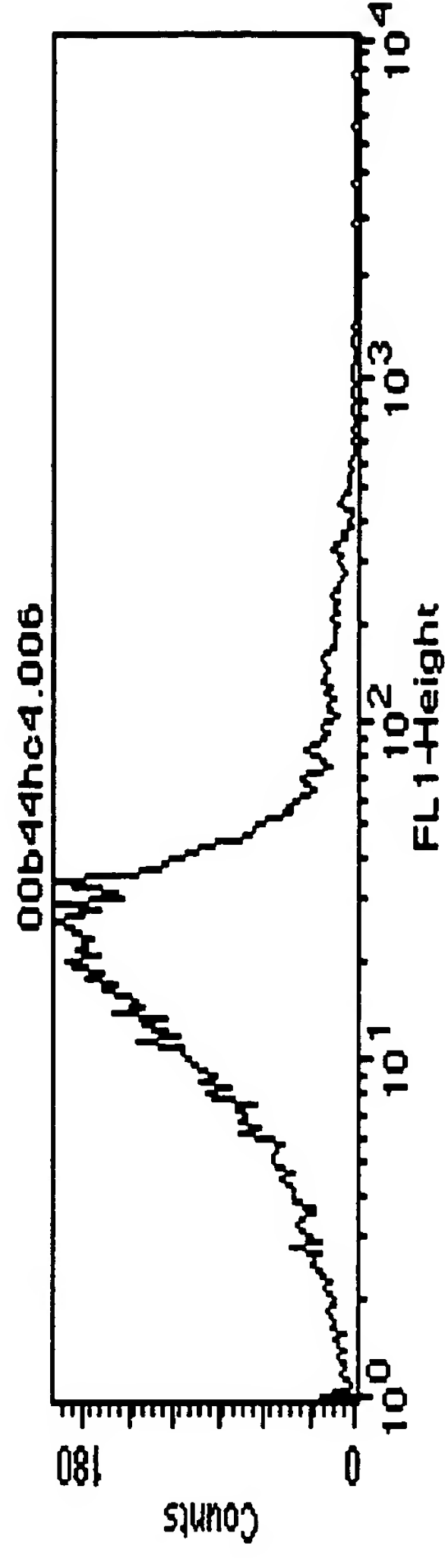


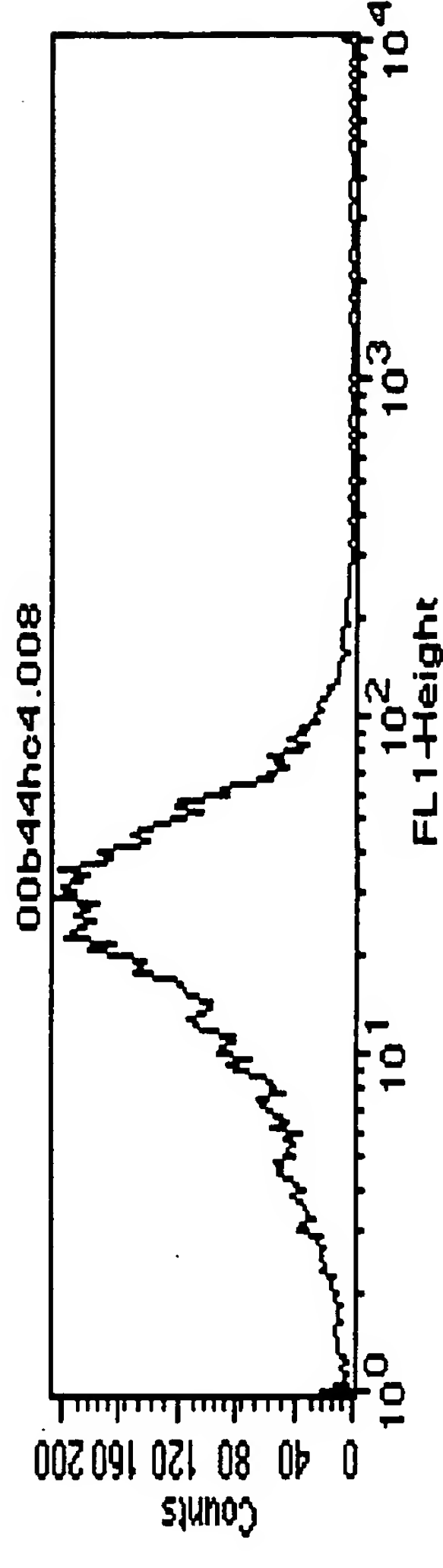
Figure 46



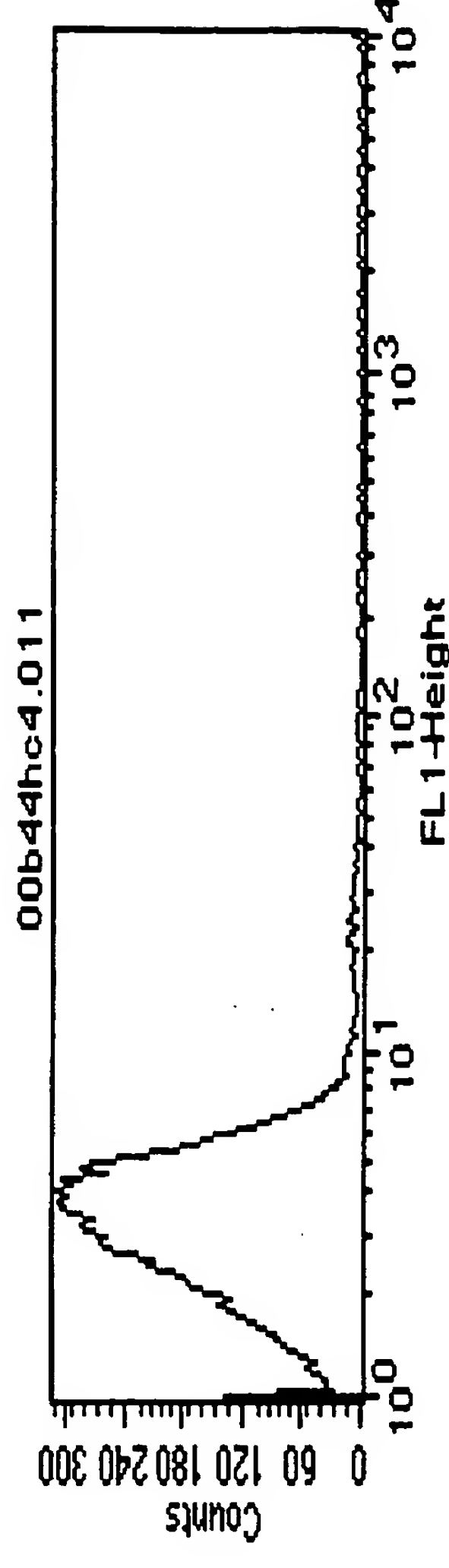
huIgG1



Pro245-Fc (0.2 µg)



Pro245-Fc (0.2 µg)
+
TRAINR-His (10µg)



Pro245-Fc (0.2 µg)
+
Pro1868-His (10µg)

Figure 47

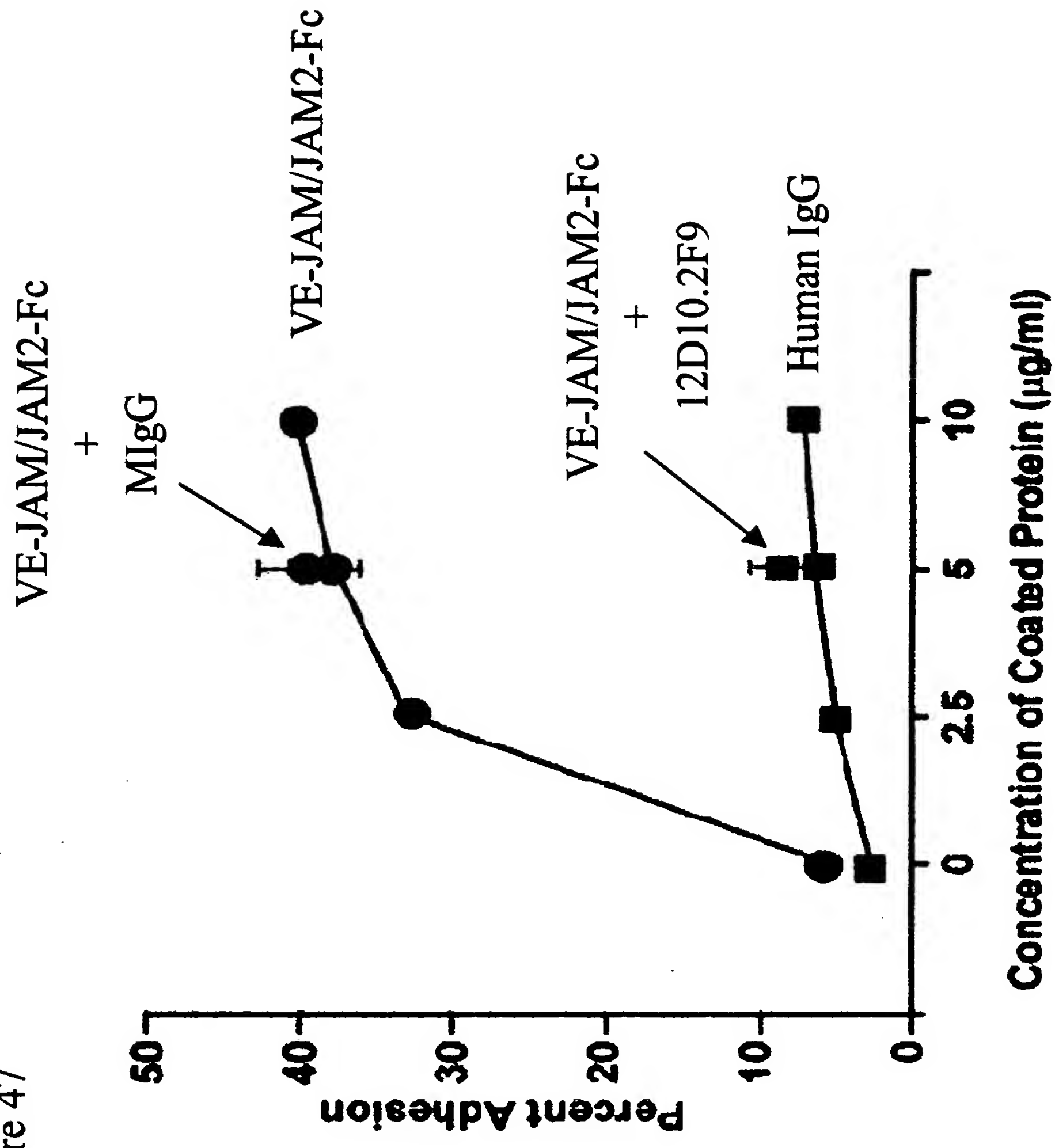


Figure 48

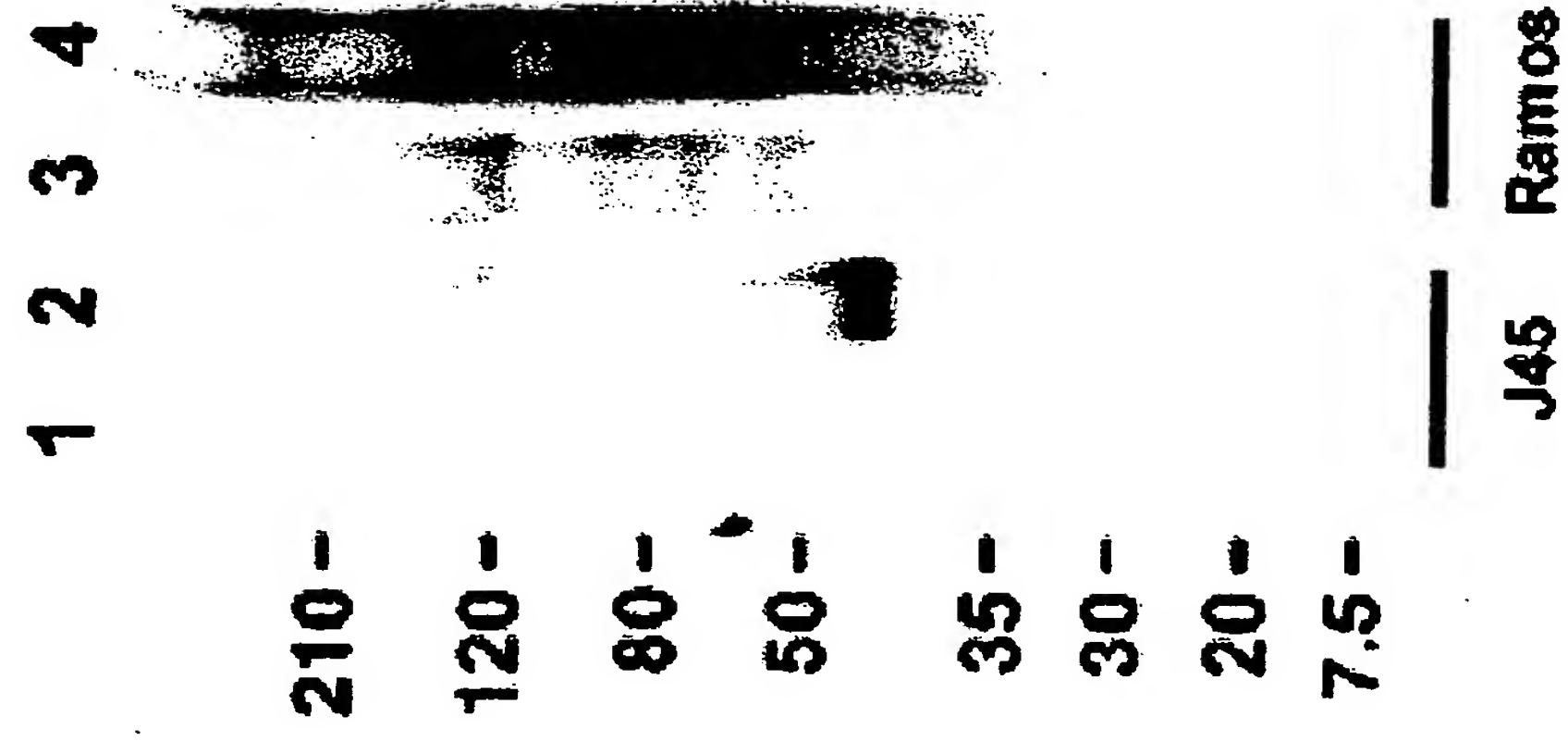


Figure 49

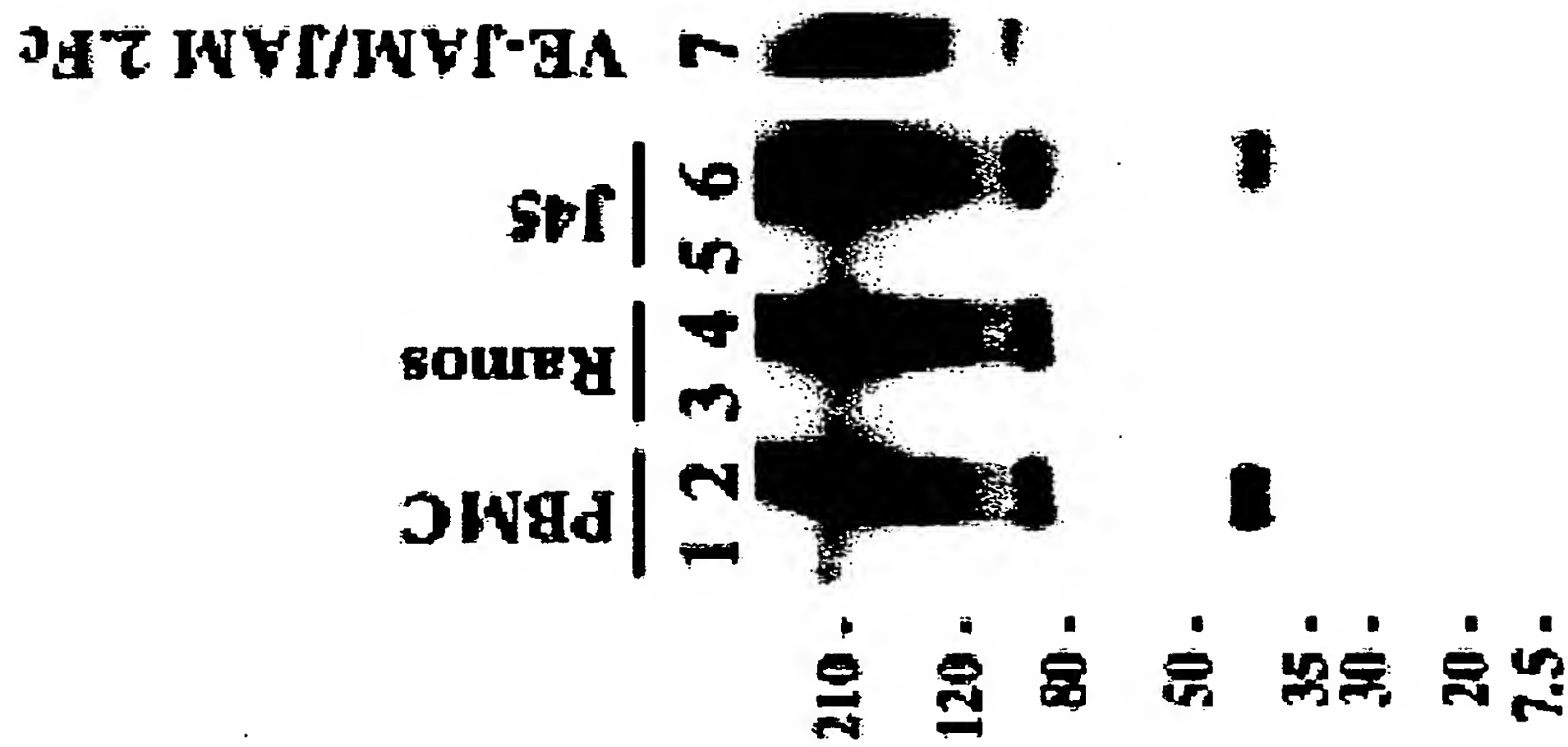


Figure 50

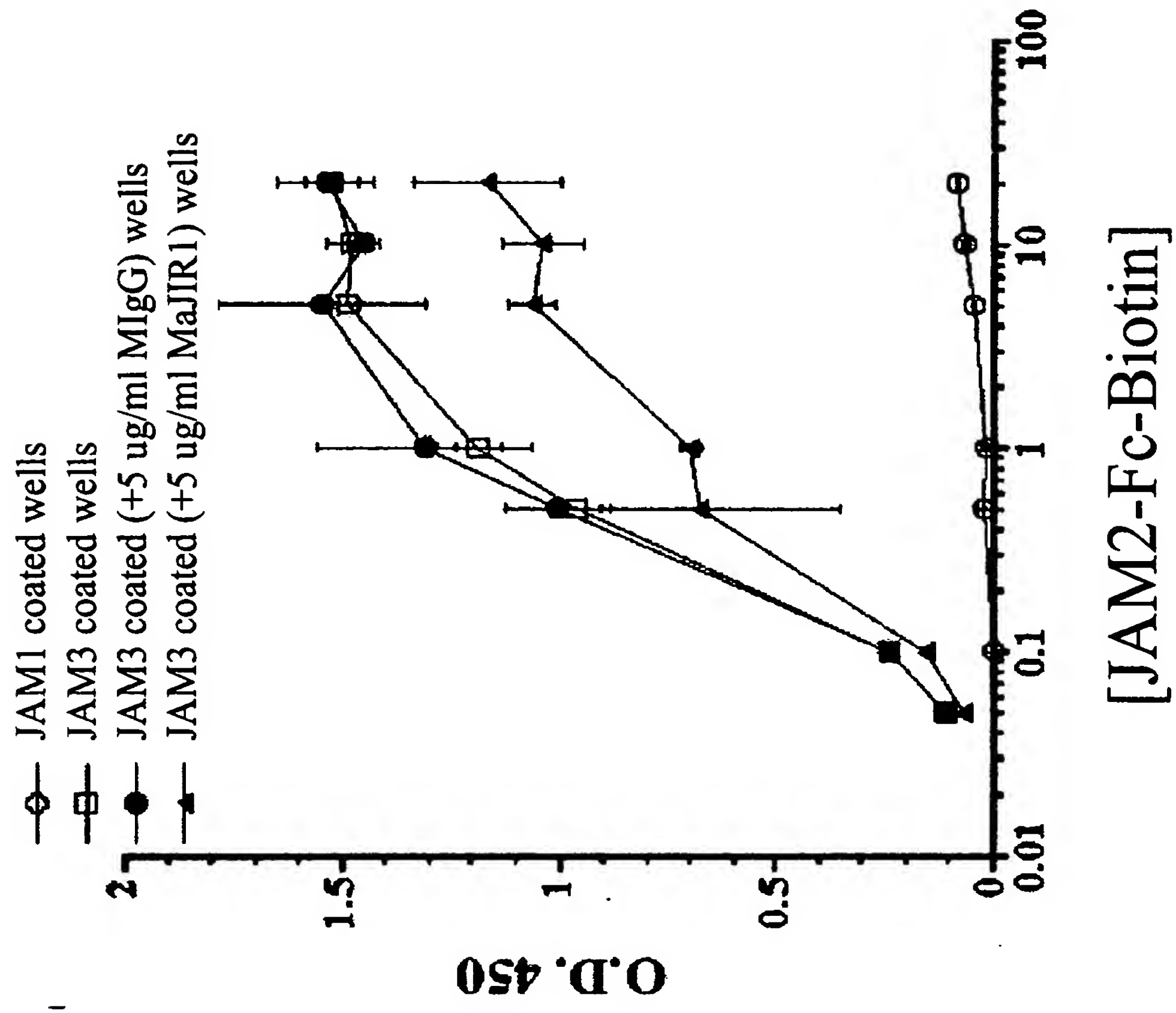


Figure 51

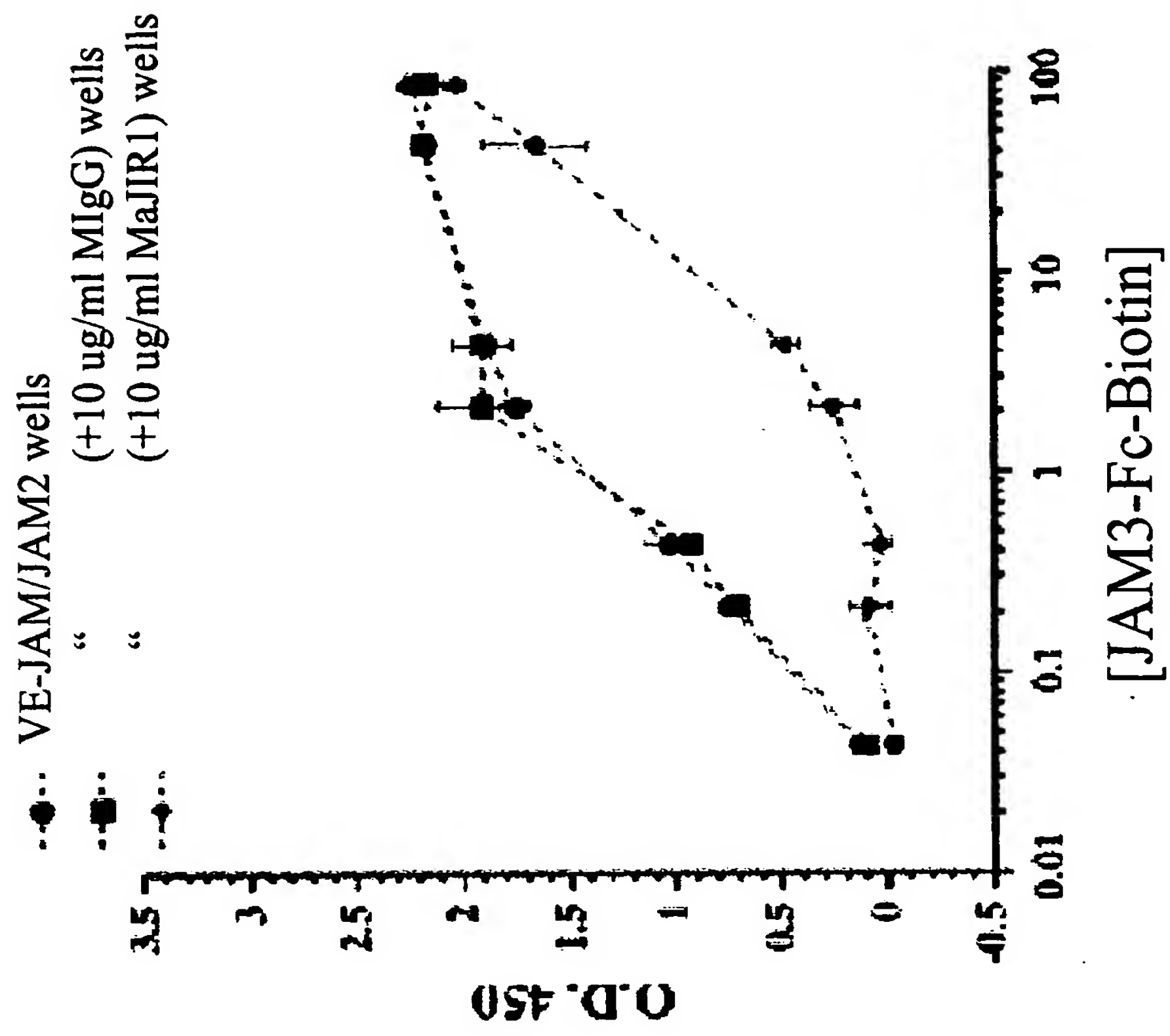


Figure 52

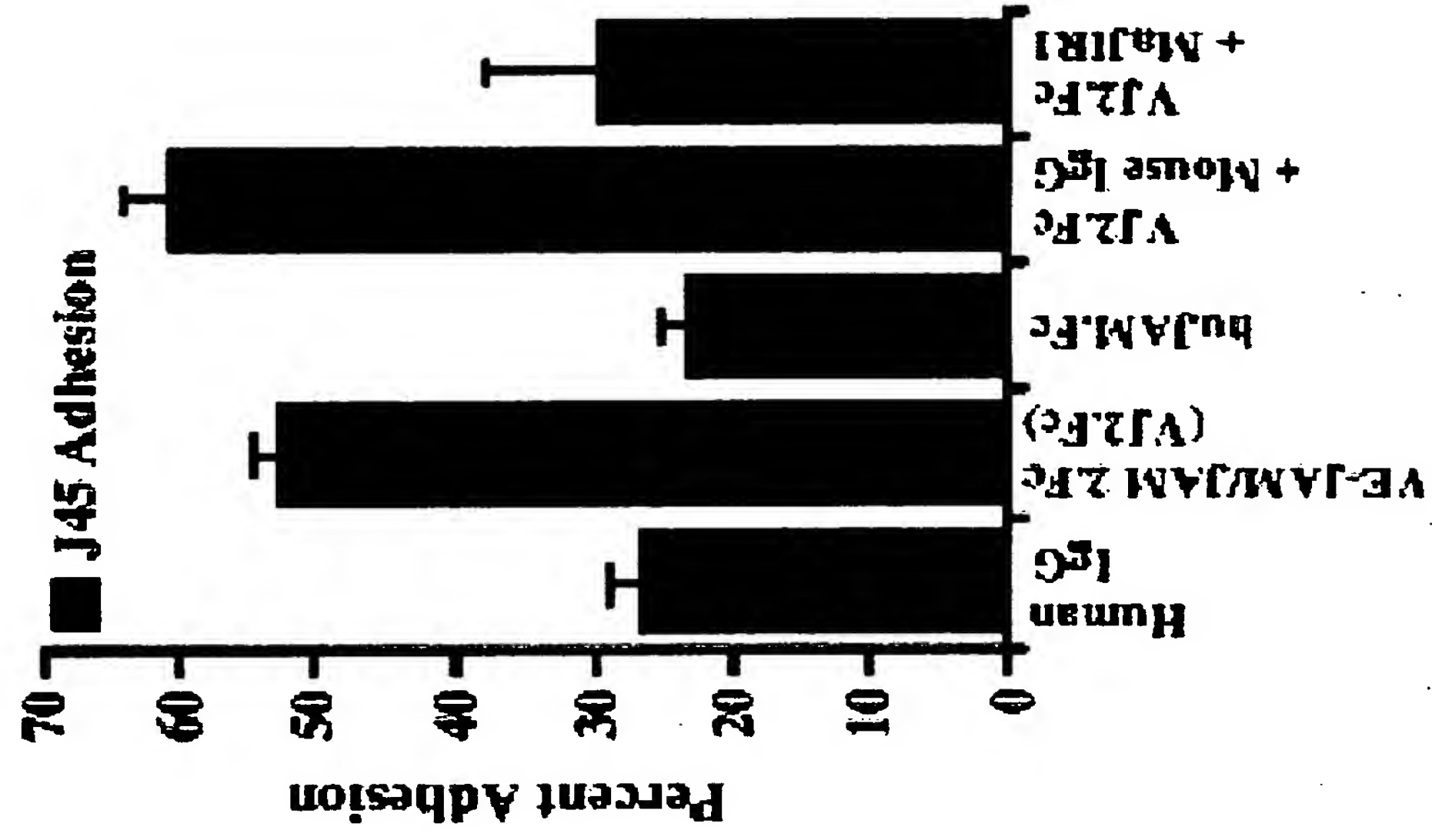


Figure 53

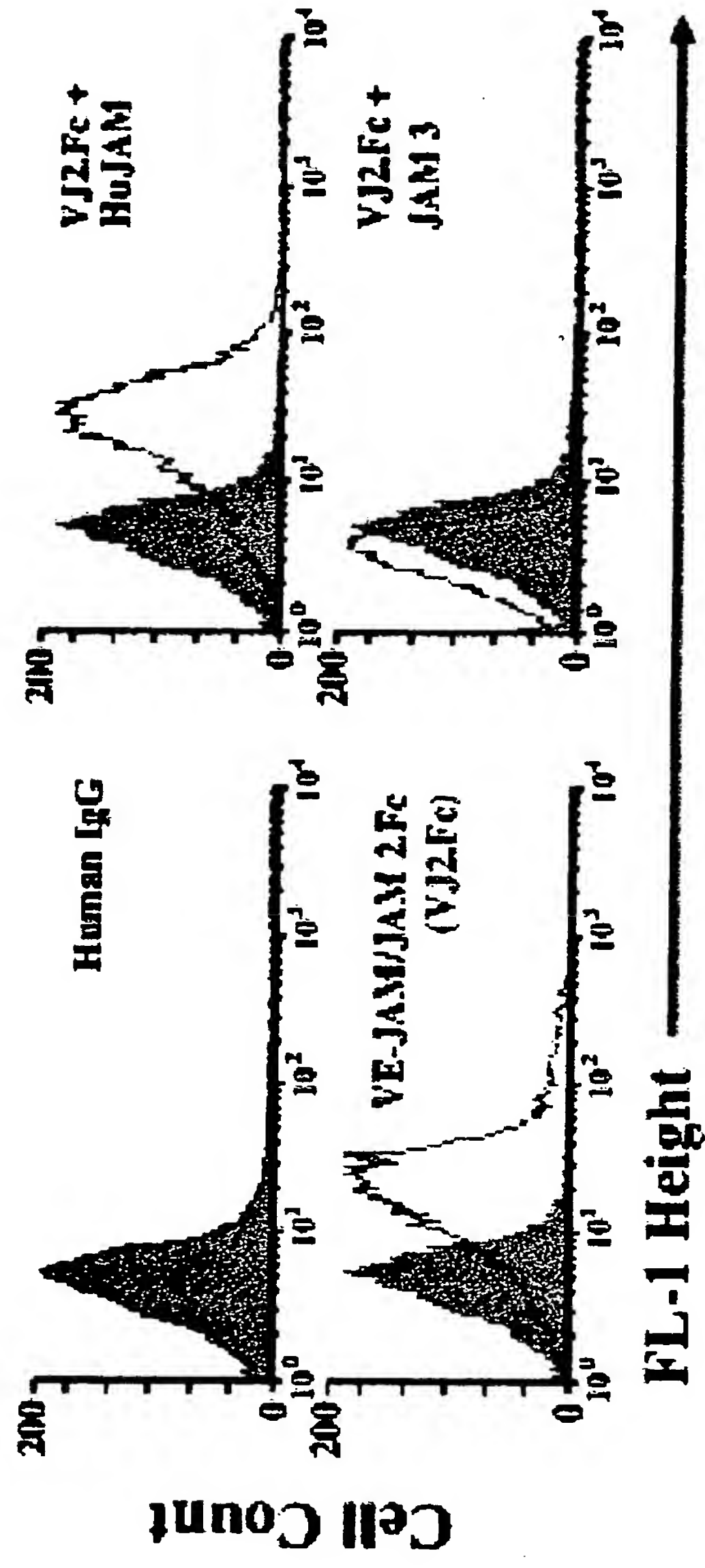


Figure 54

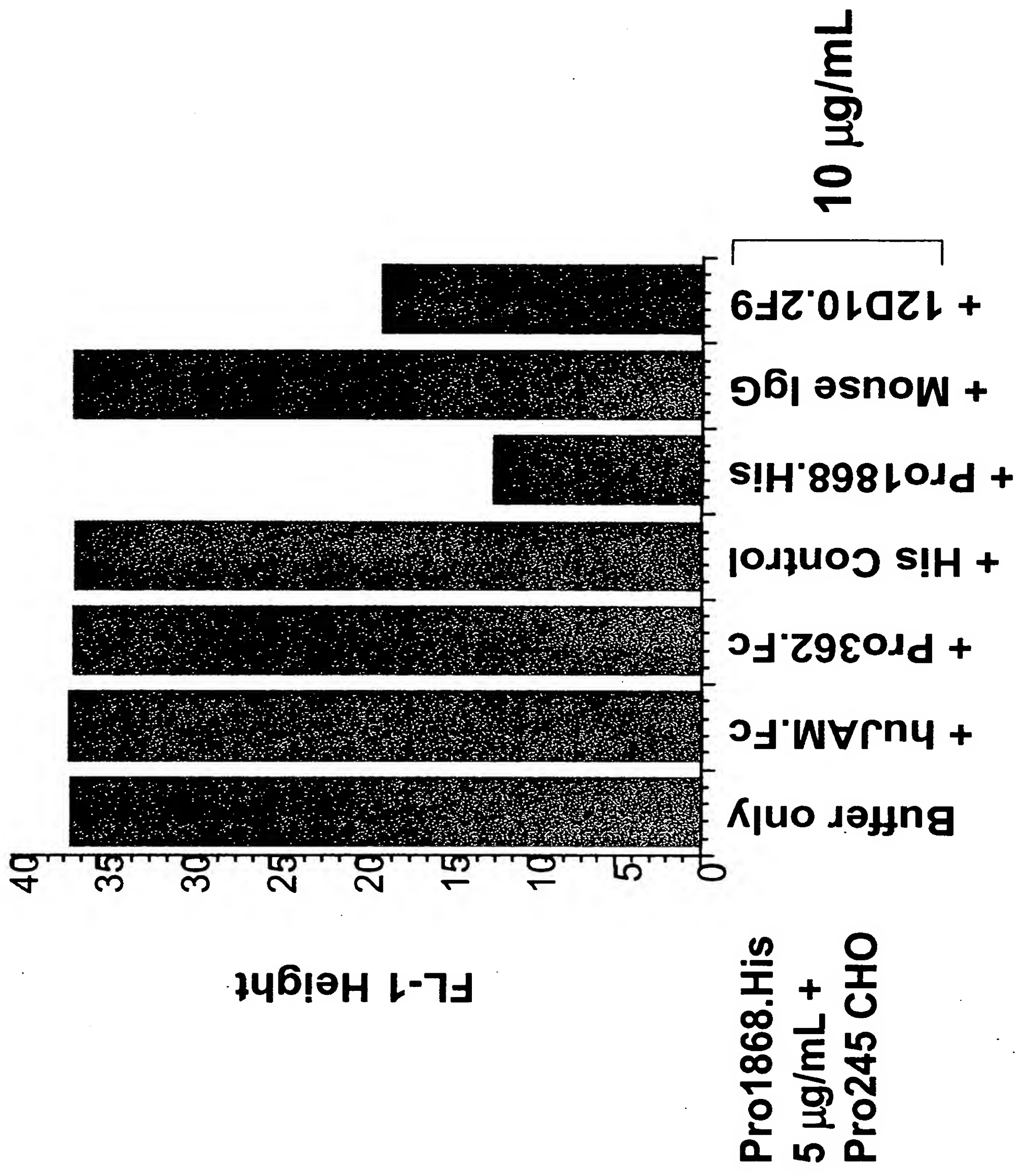
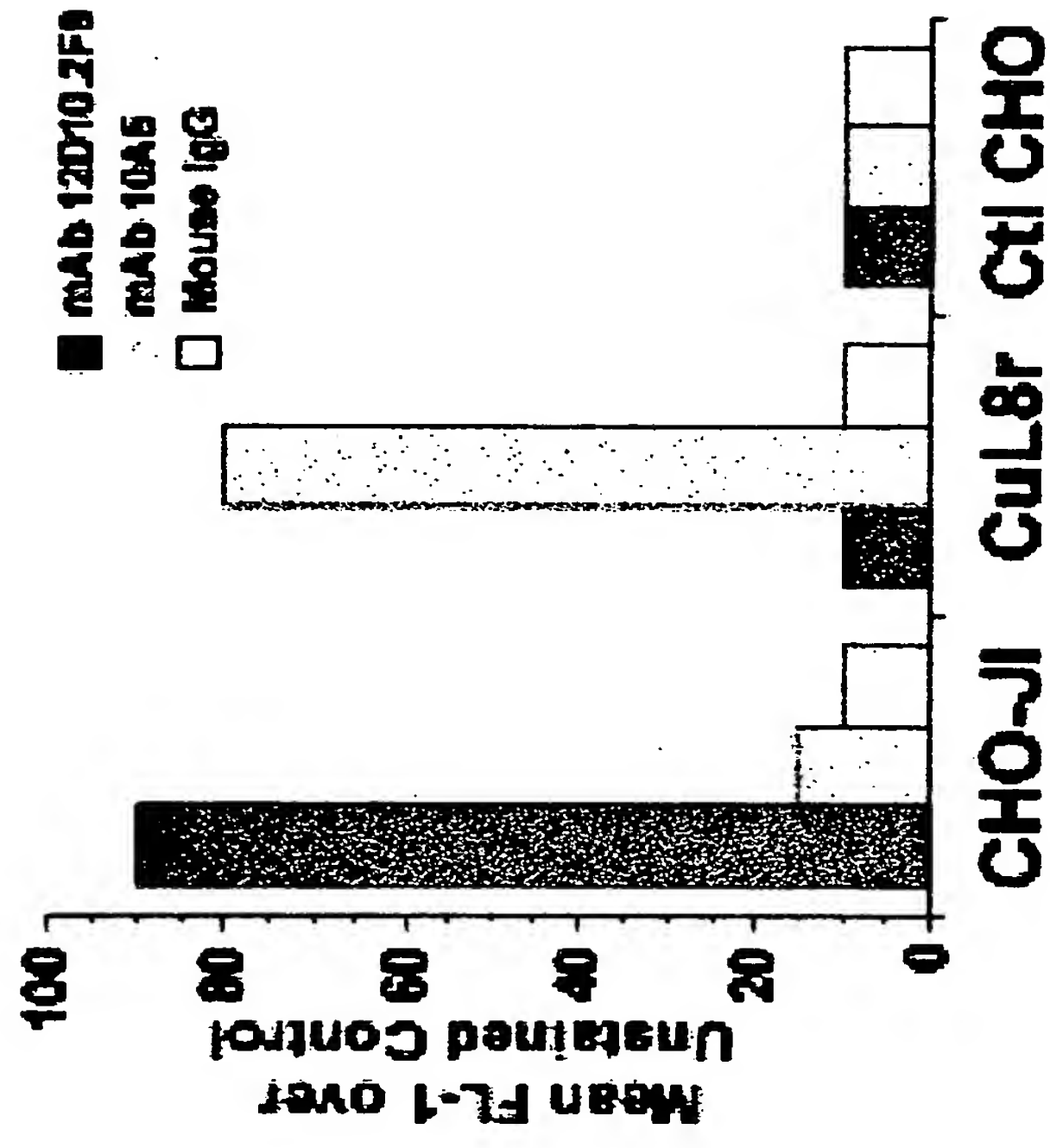


Figure 55



uterus
trachea
thyroid
stomach
spinal chord
prostate
mammary gland
lymph node
brain
bone marrow.
bladder
adrenal gland

brain
heart
sk. musc.
colon
thymus
spleen
kidney
liver
small int.
placenta
lung
PBL

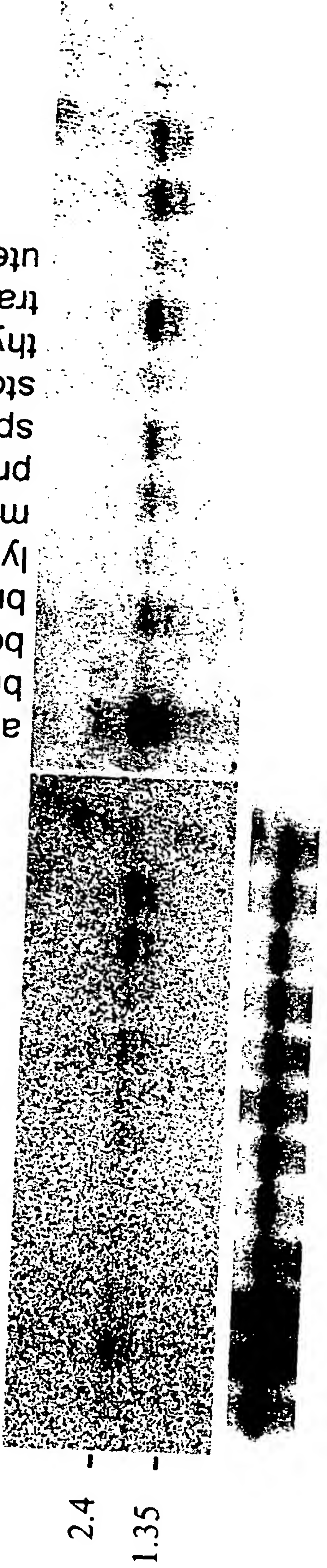
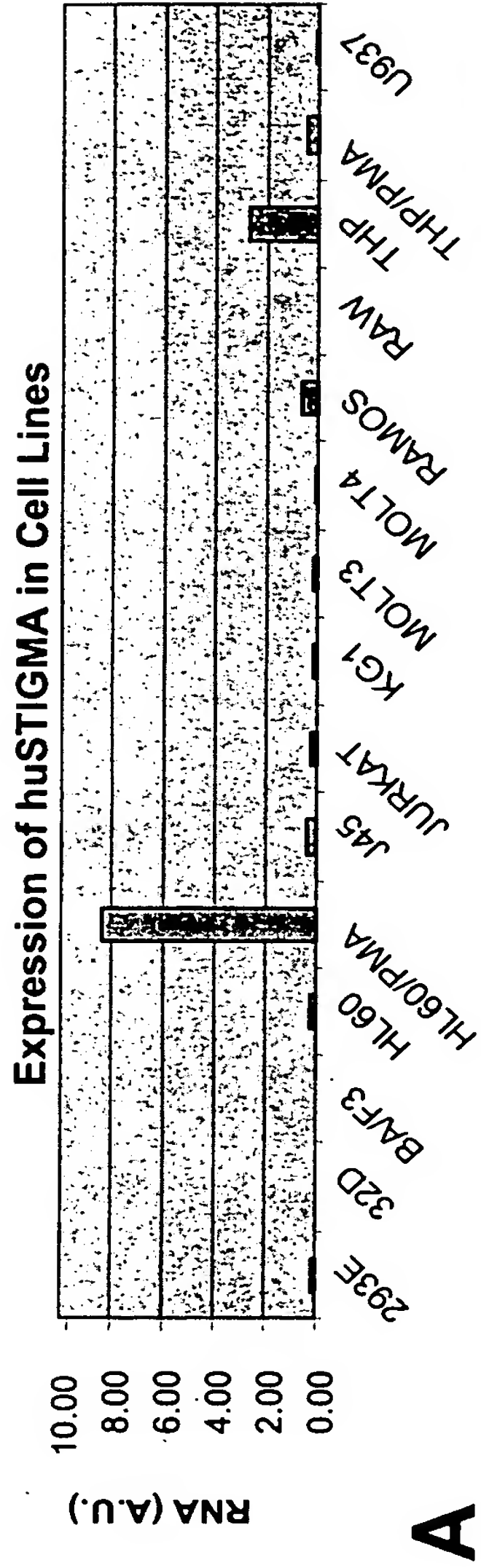
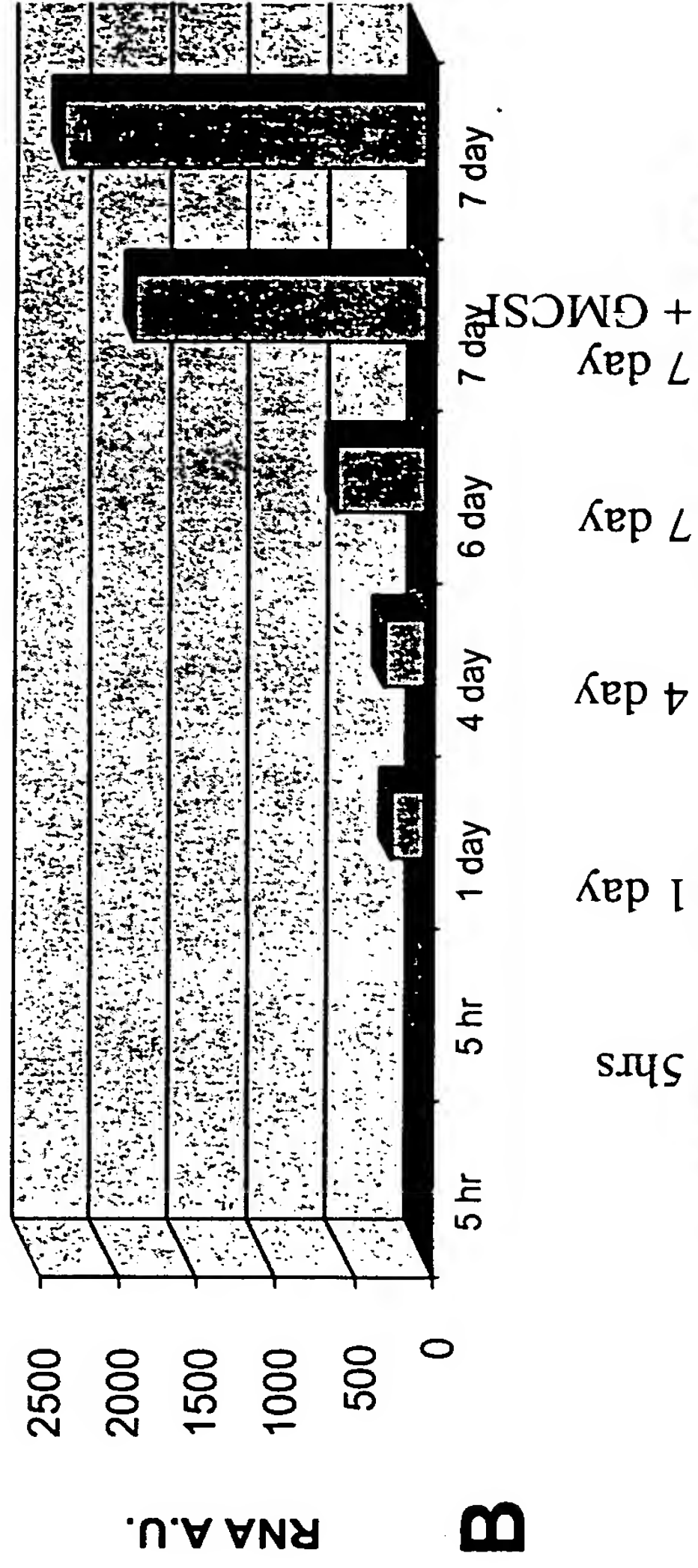


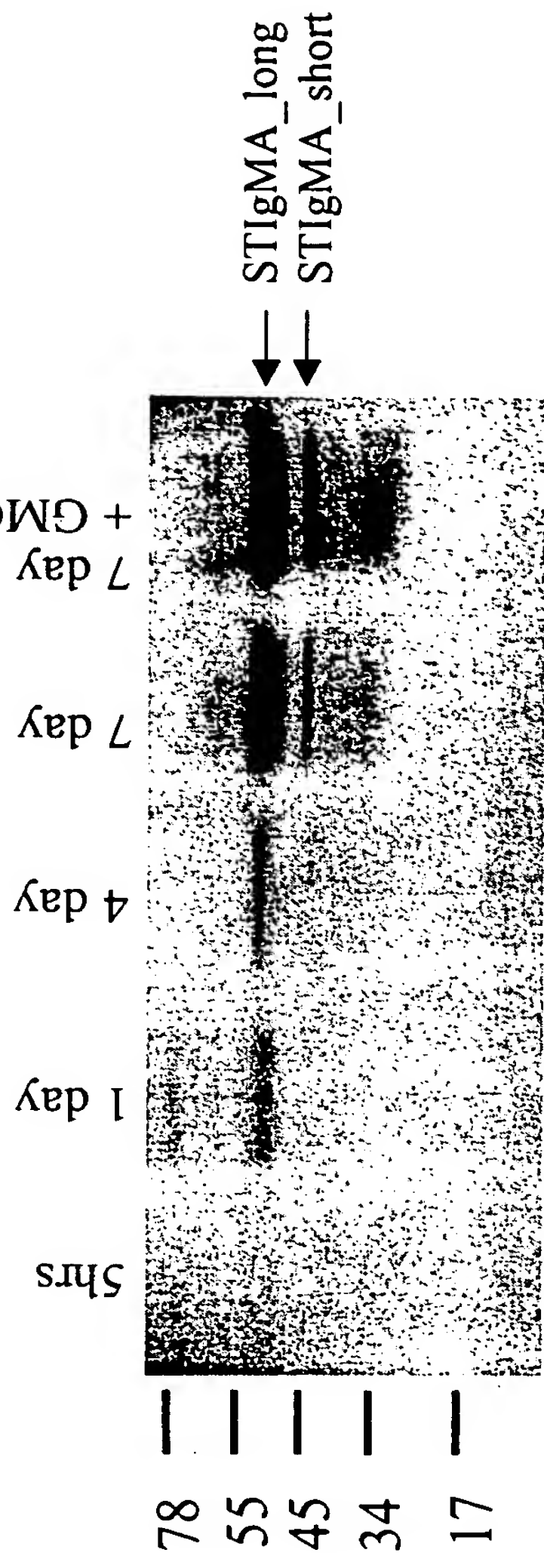
Fig. 57



A



B



C

Fig. 58

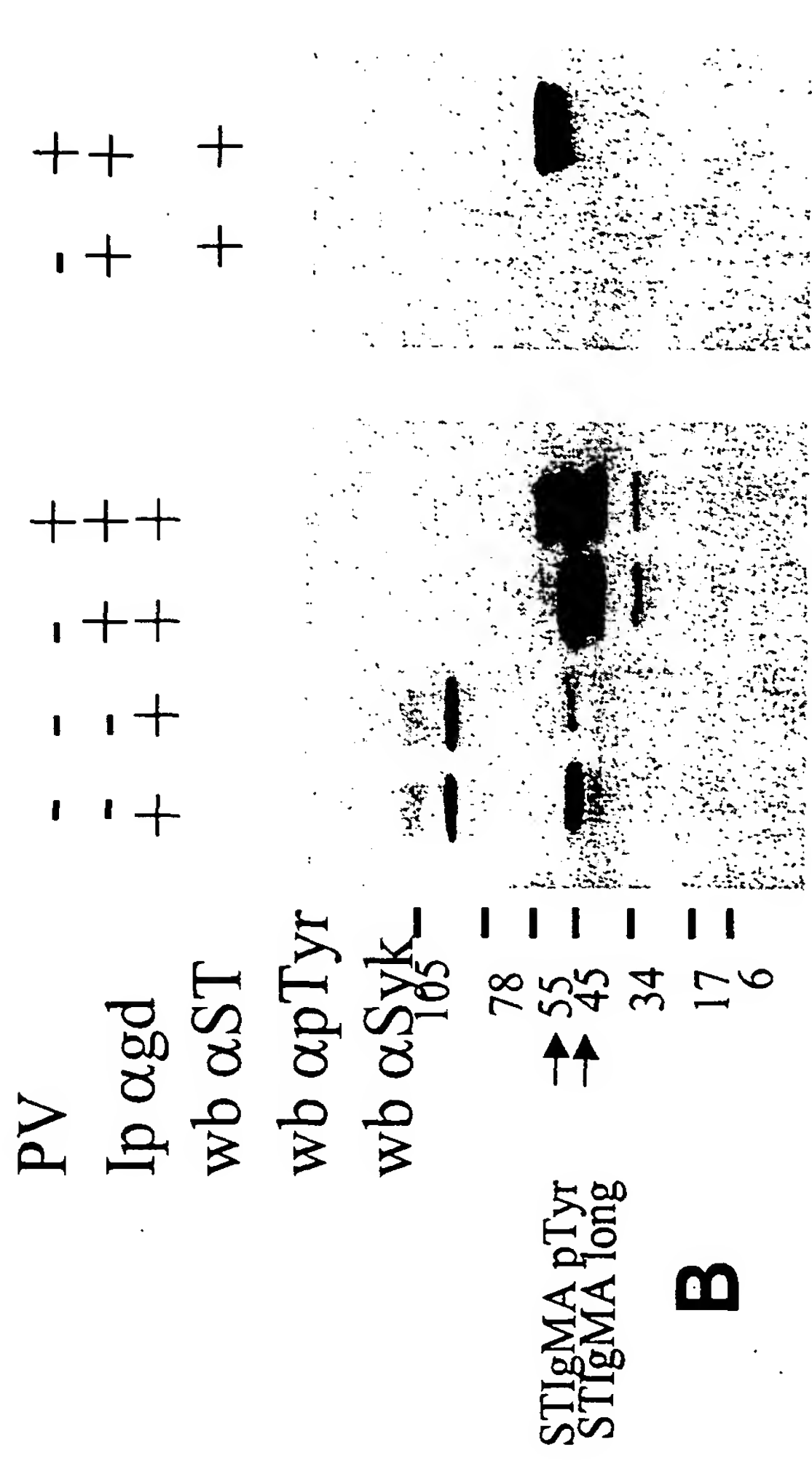
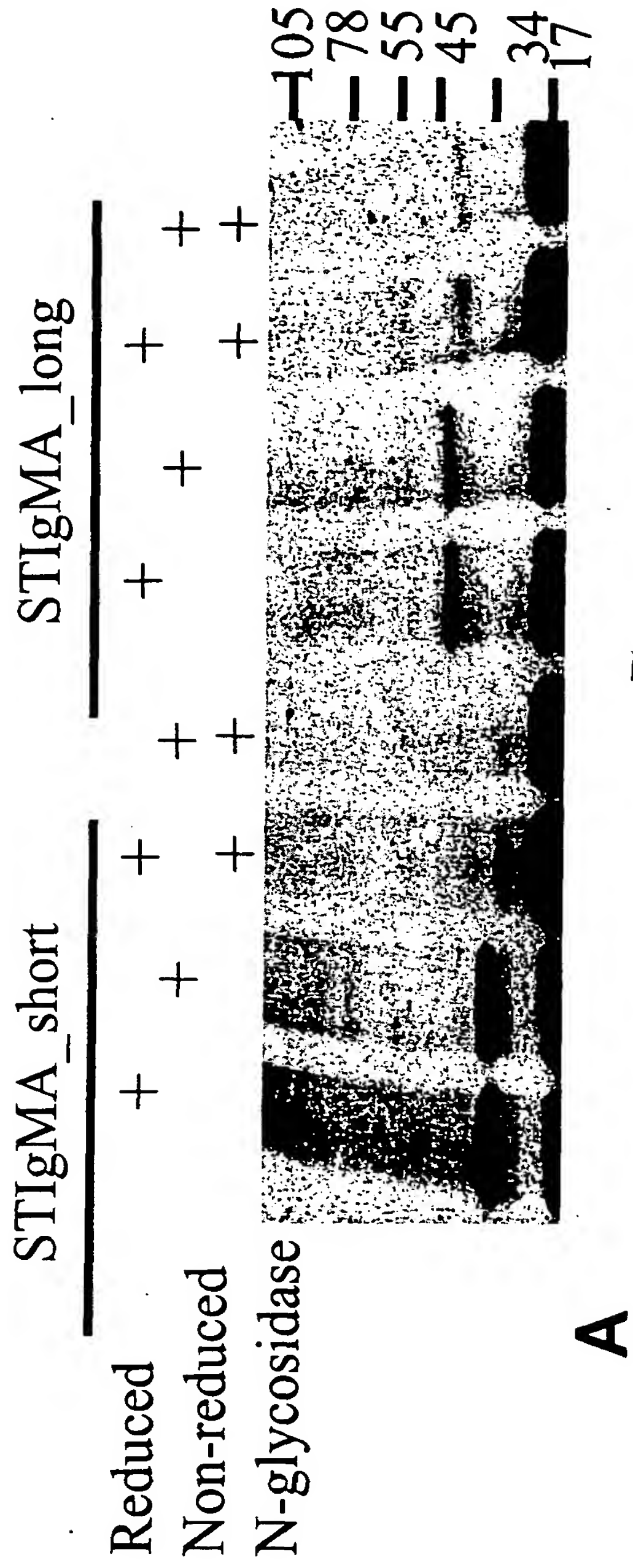
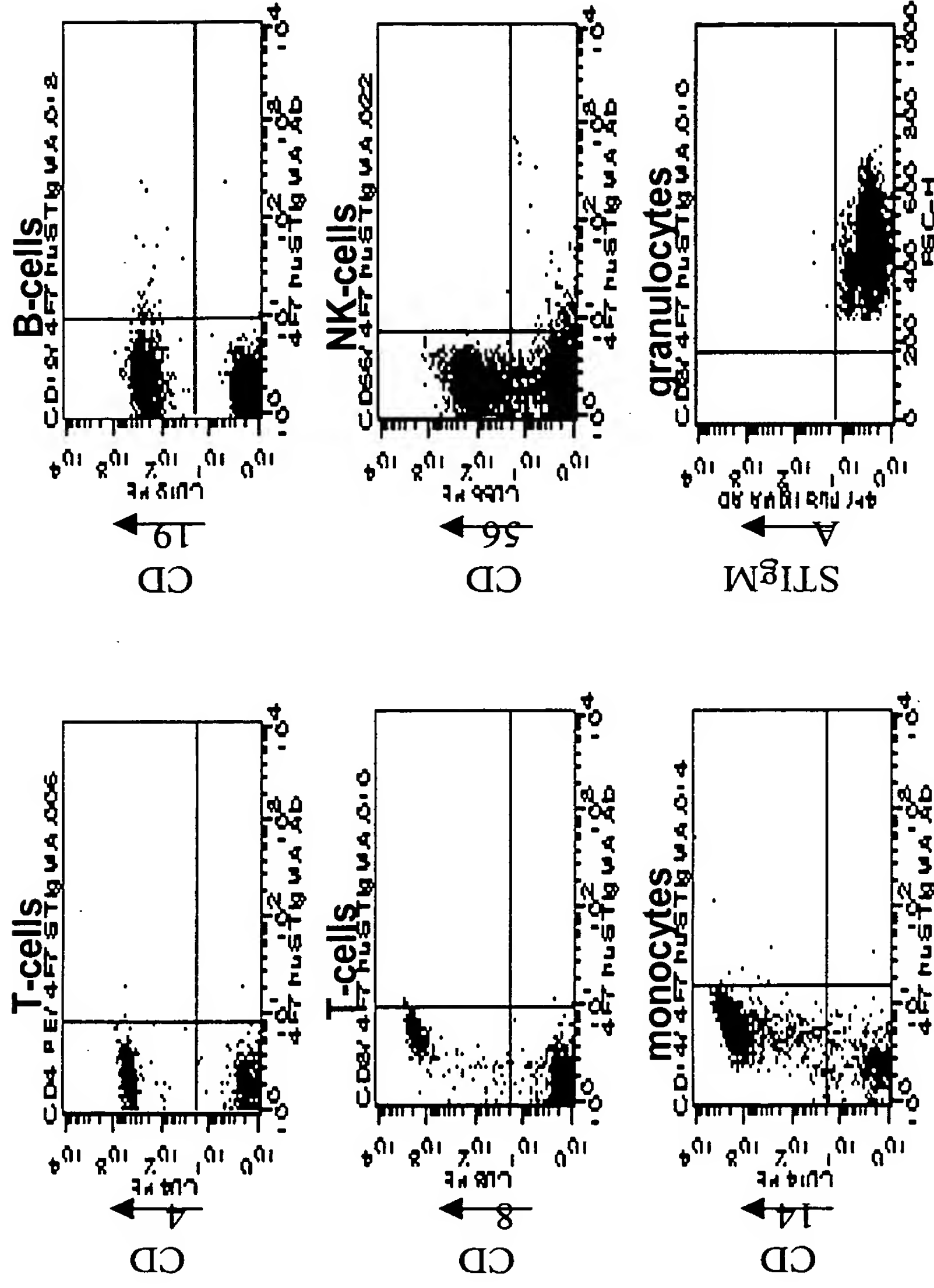
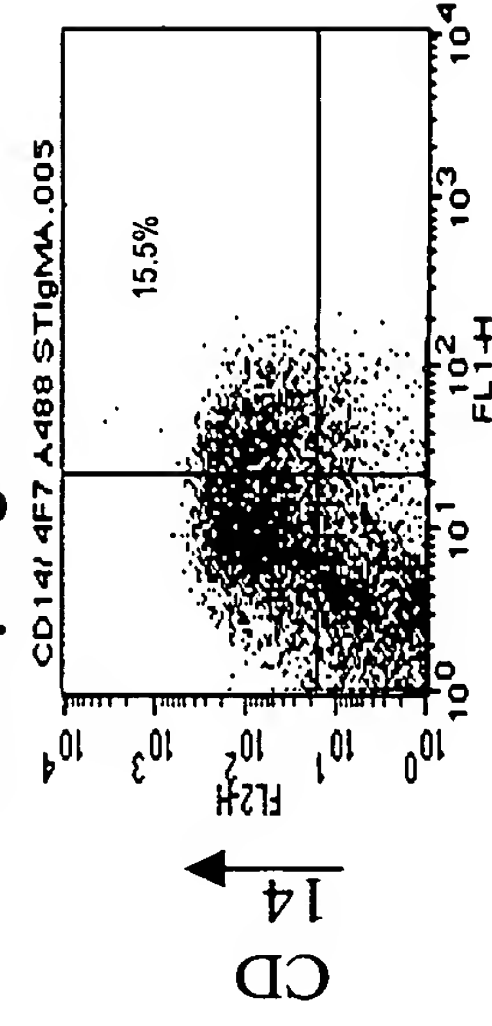


Fig. 59



monocyte-derived
macrophages



Anti-STIgMA (4F7)

Fig. 60

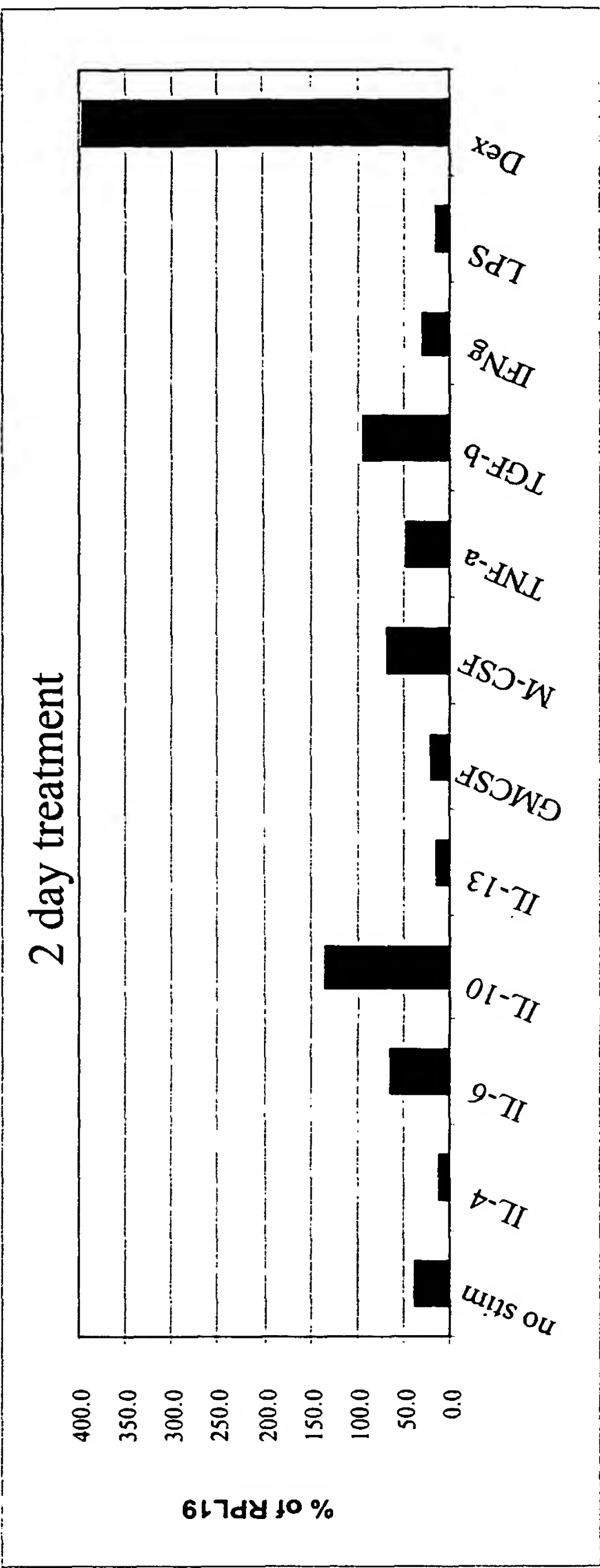
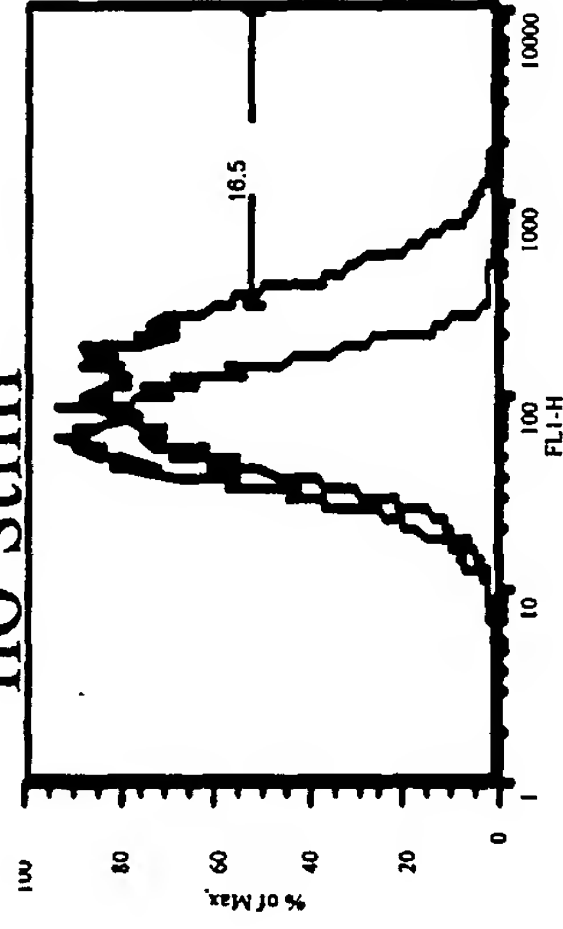


Fig. 61A

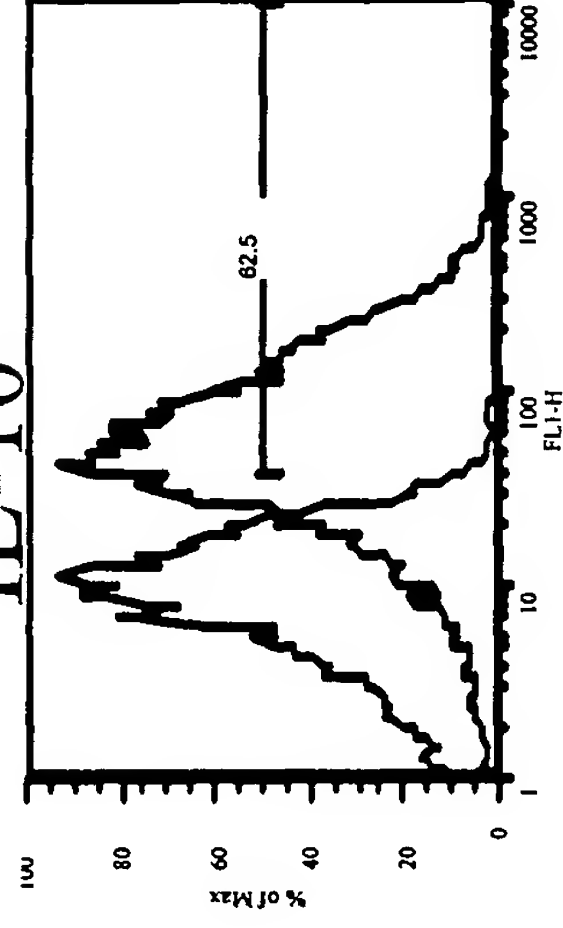
mIgG1-AF-488

no stim

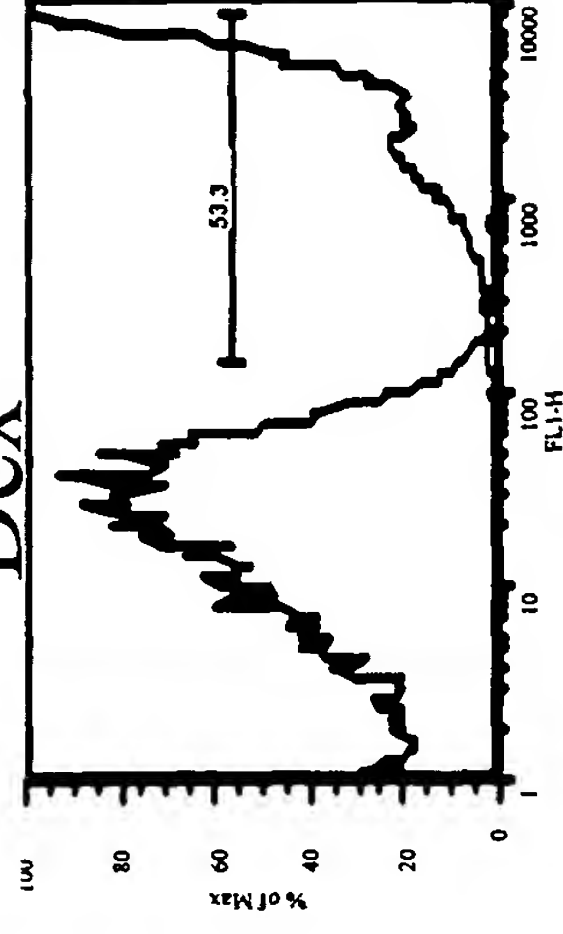


hJAM4-AF-488

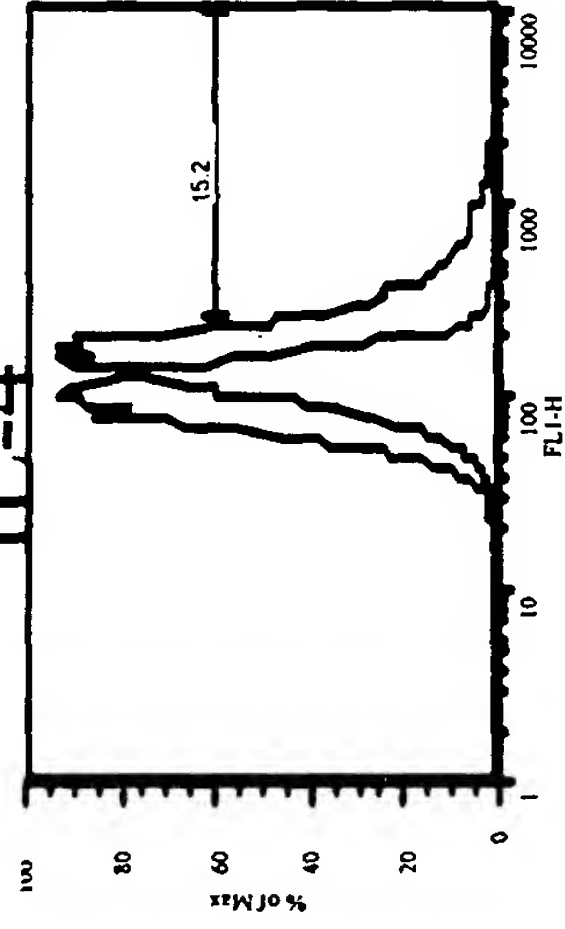
IL-10



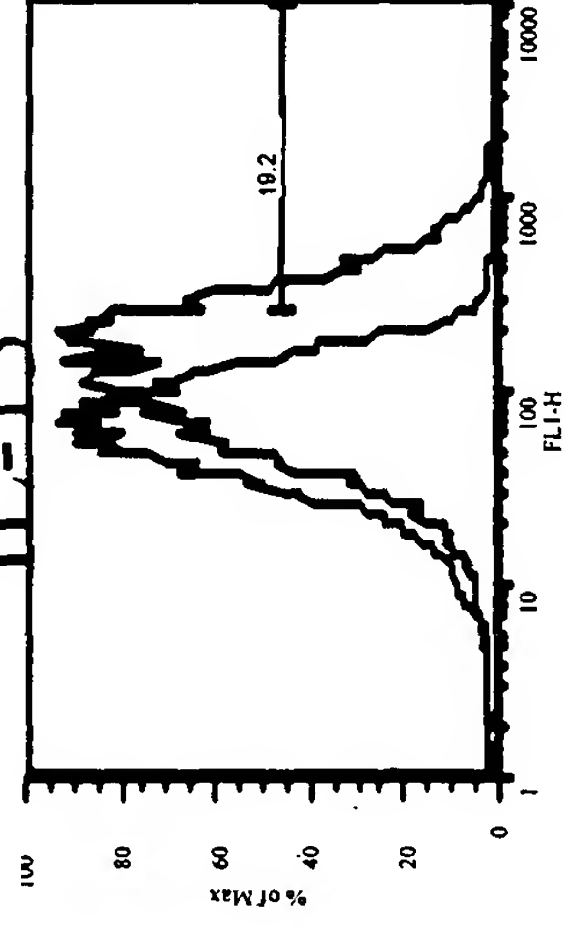
Dex



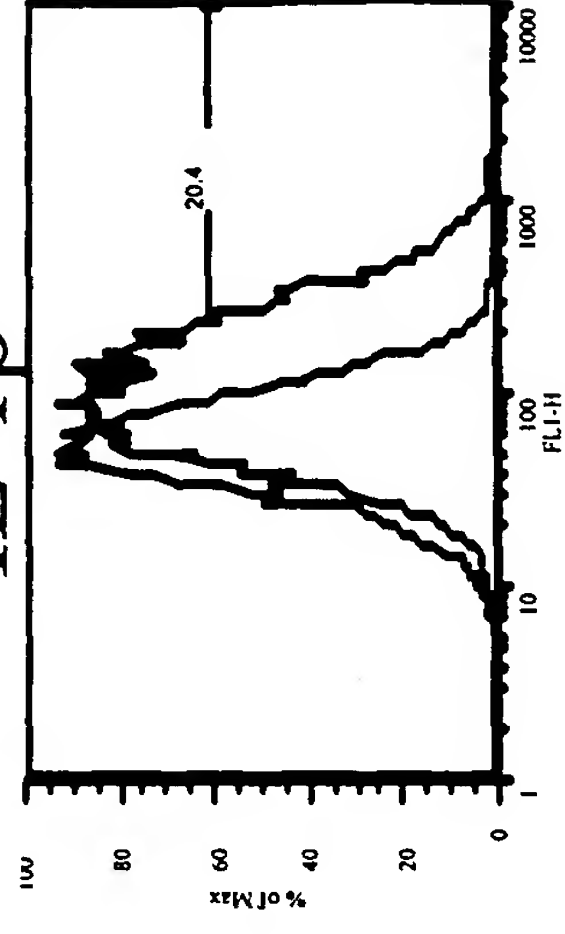
IL-4



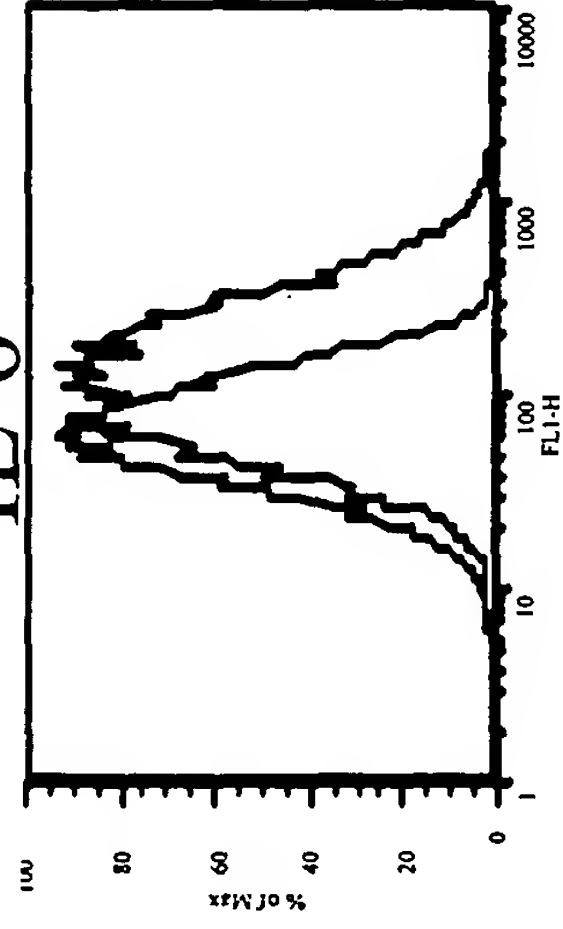
IL-13



IL-1 β



IL-6



LPS

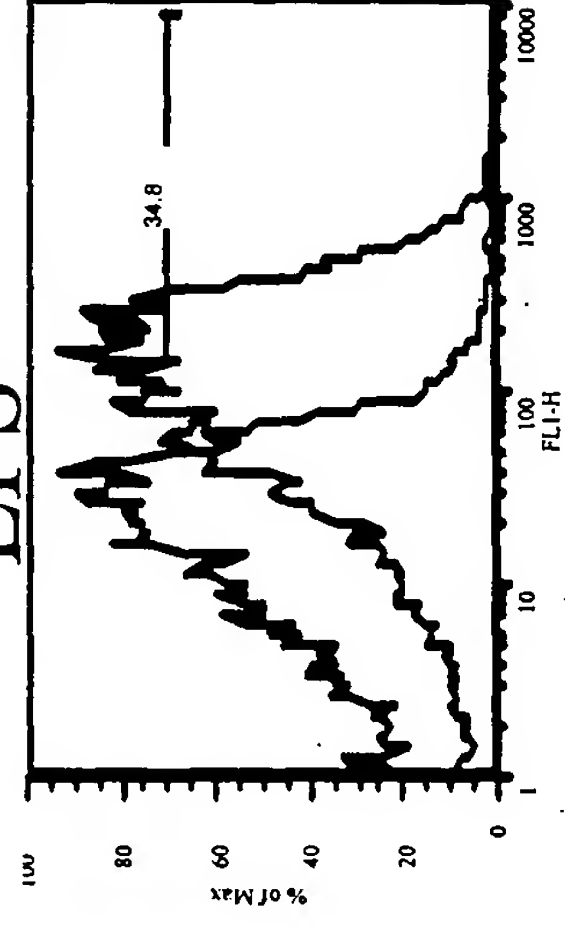


Fig. 61B

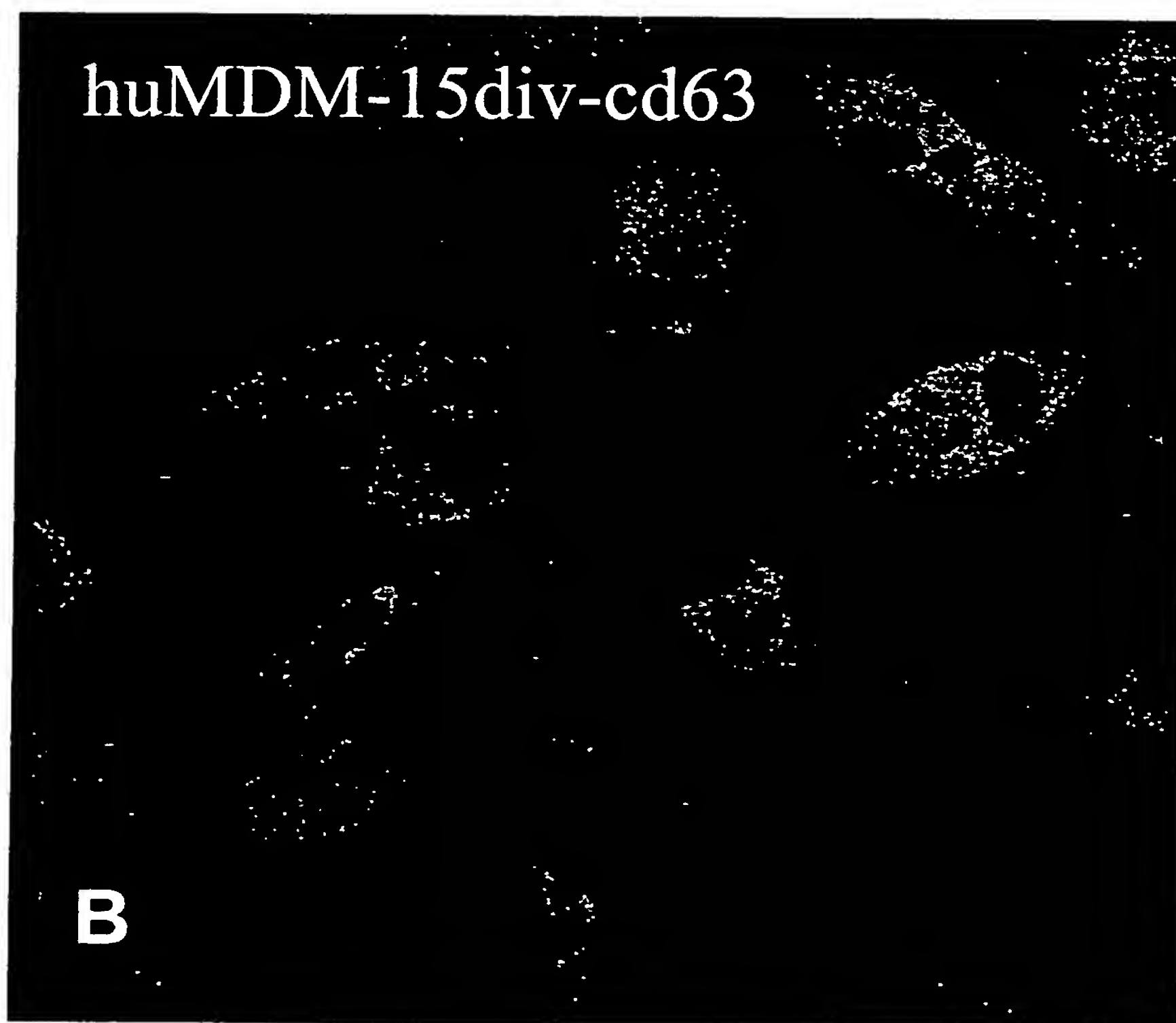
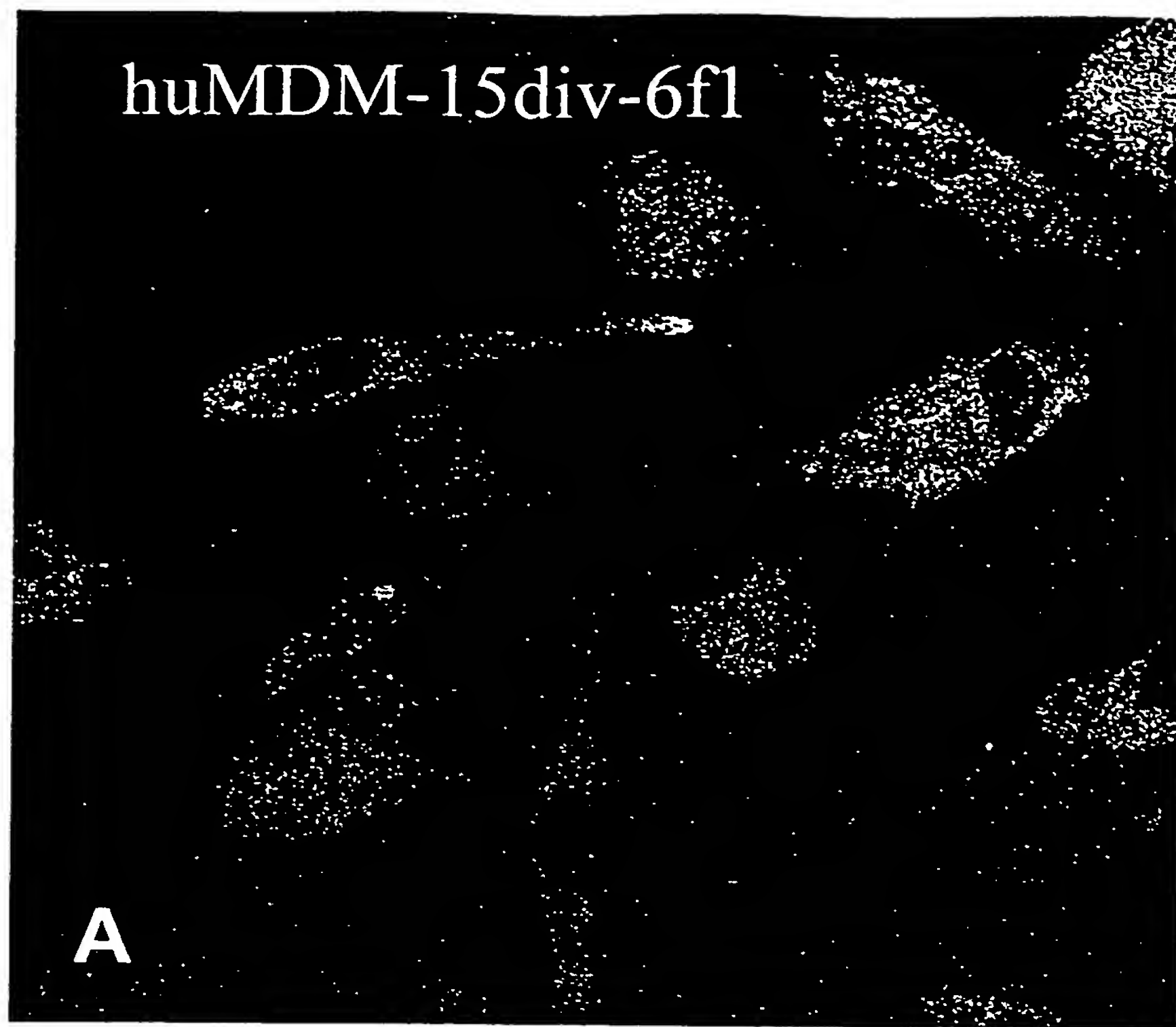


Fig.62

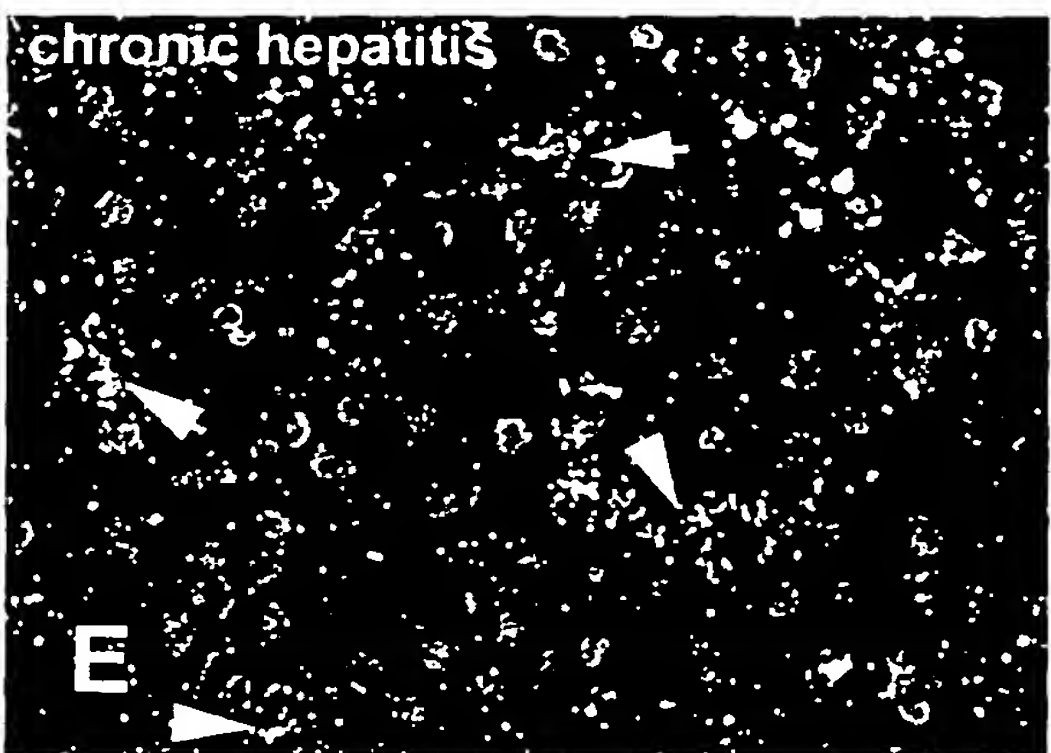
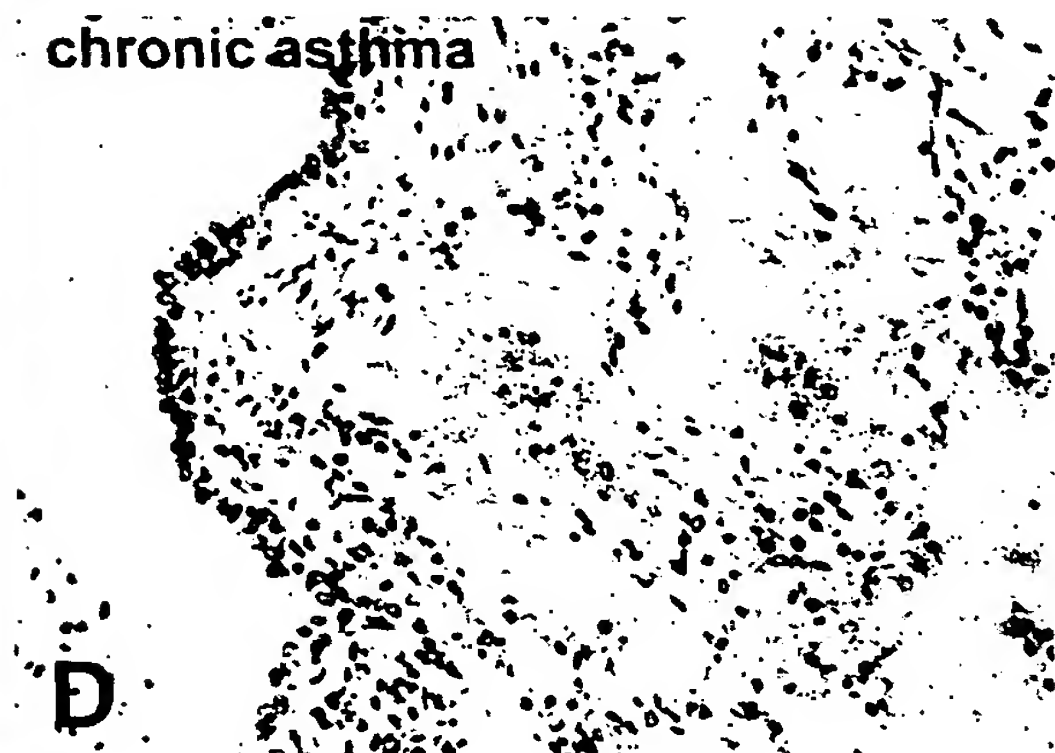
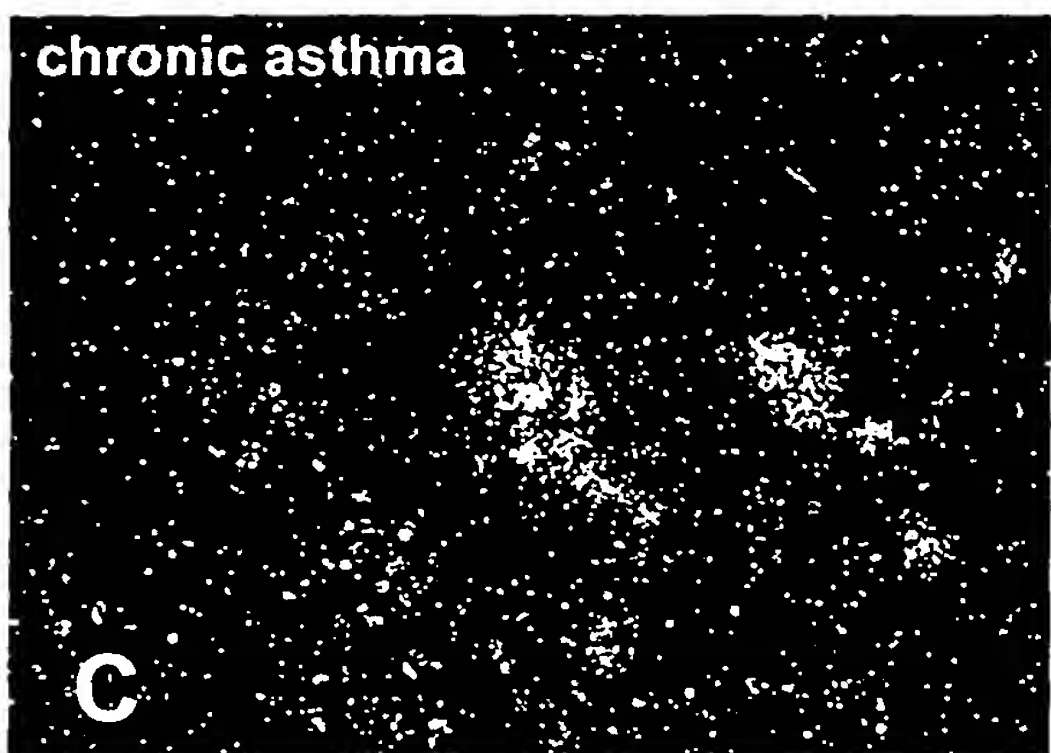
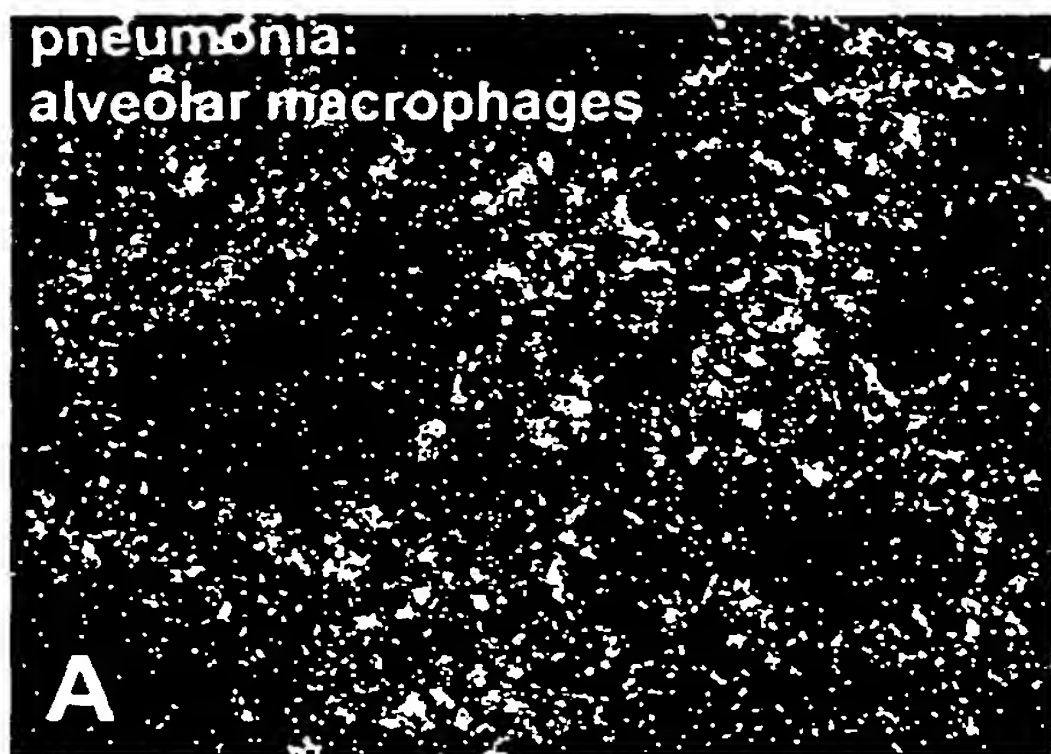


Fig. 63

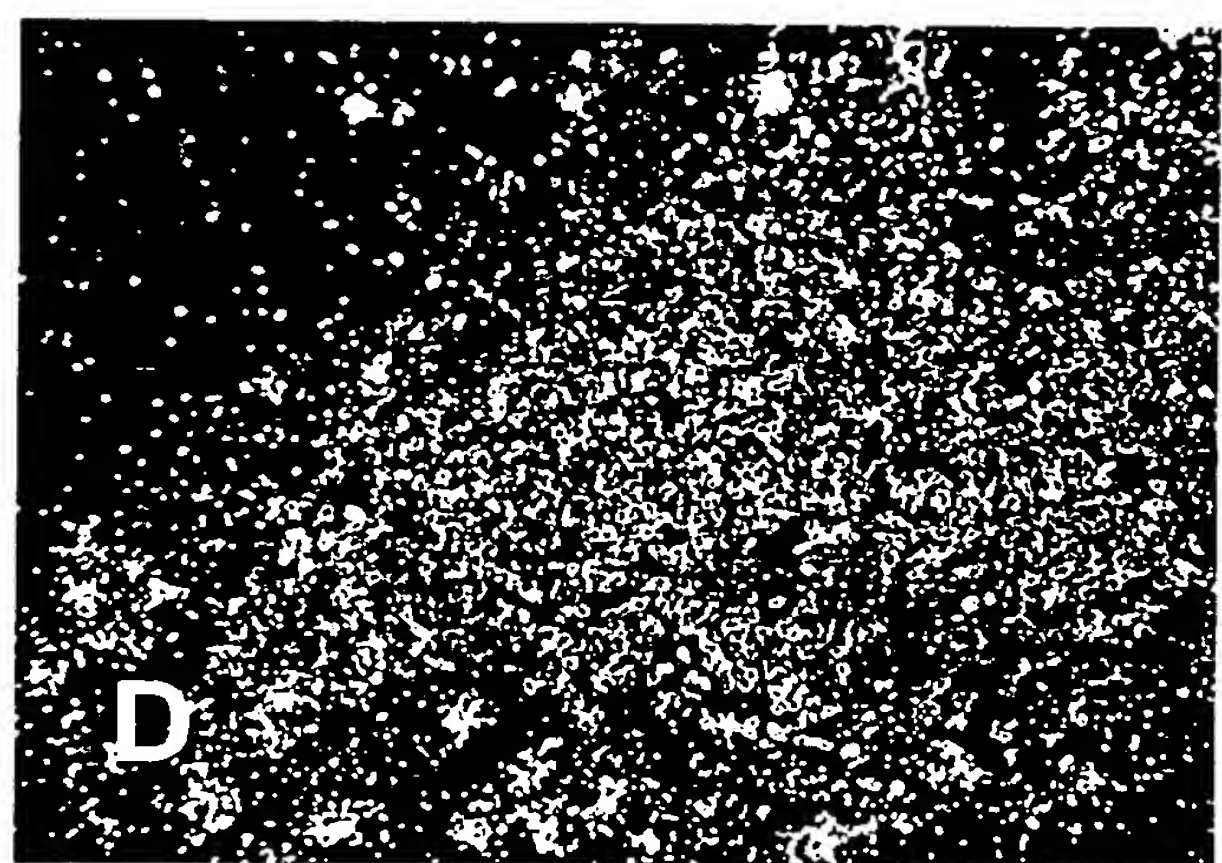
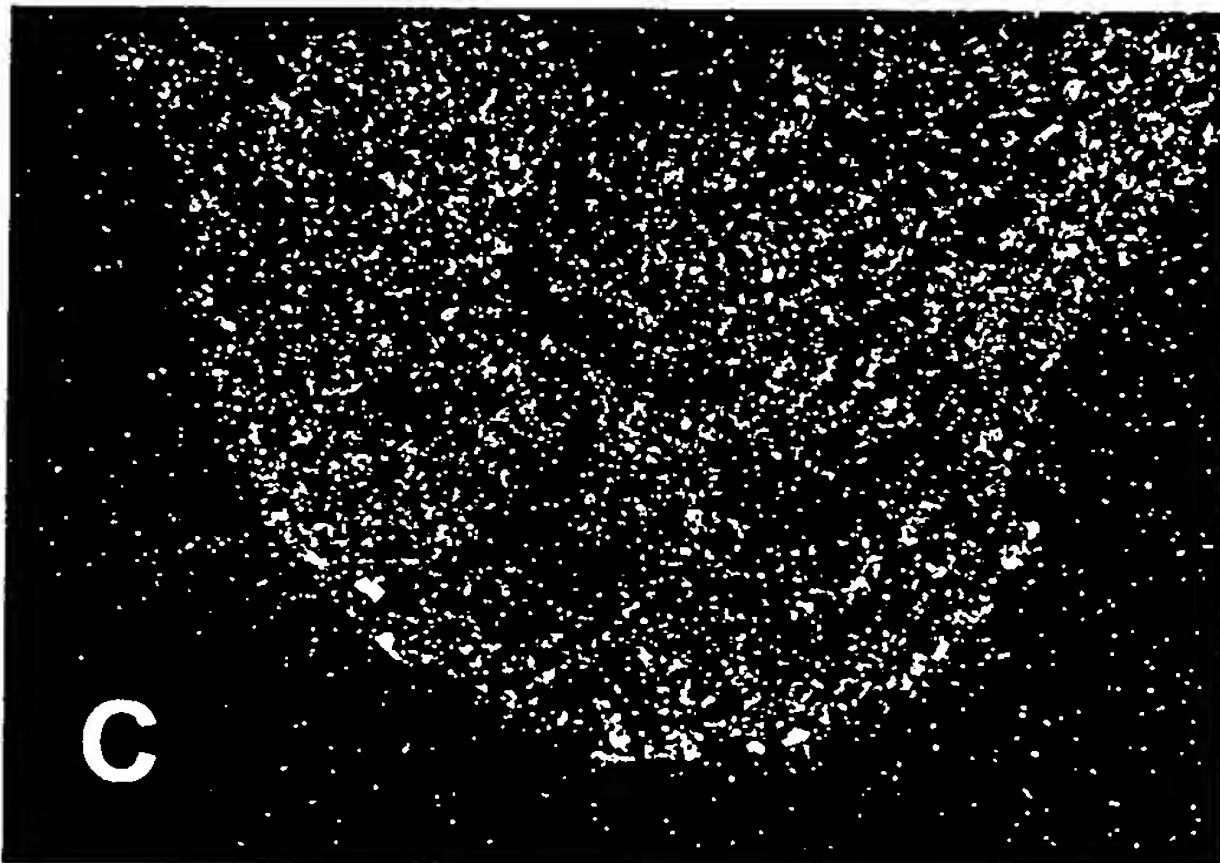
Normal

Osteoarthritis



A

B



C

D

Fig. 64

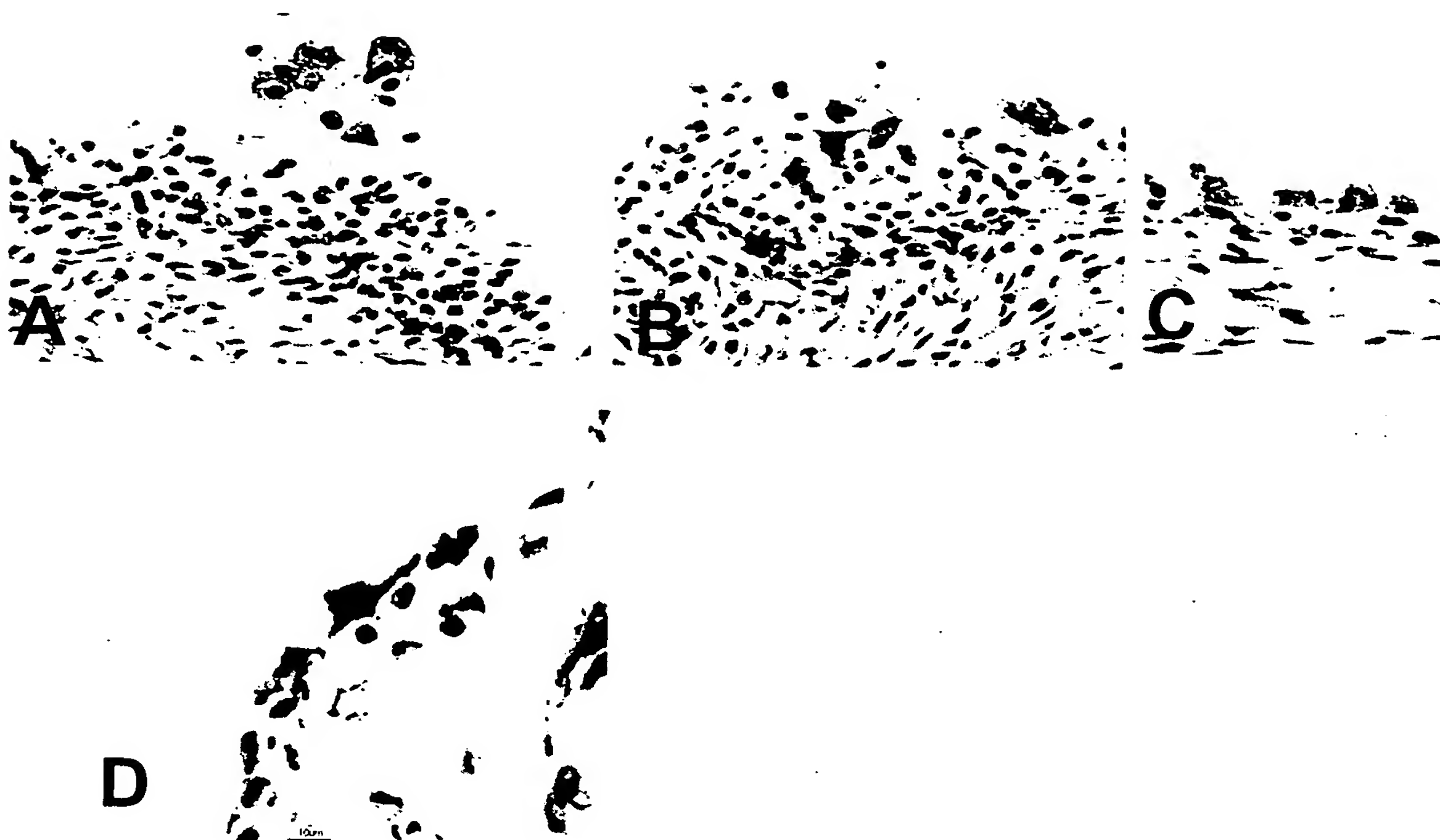


Fig. 65

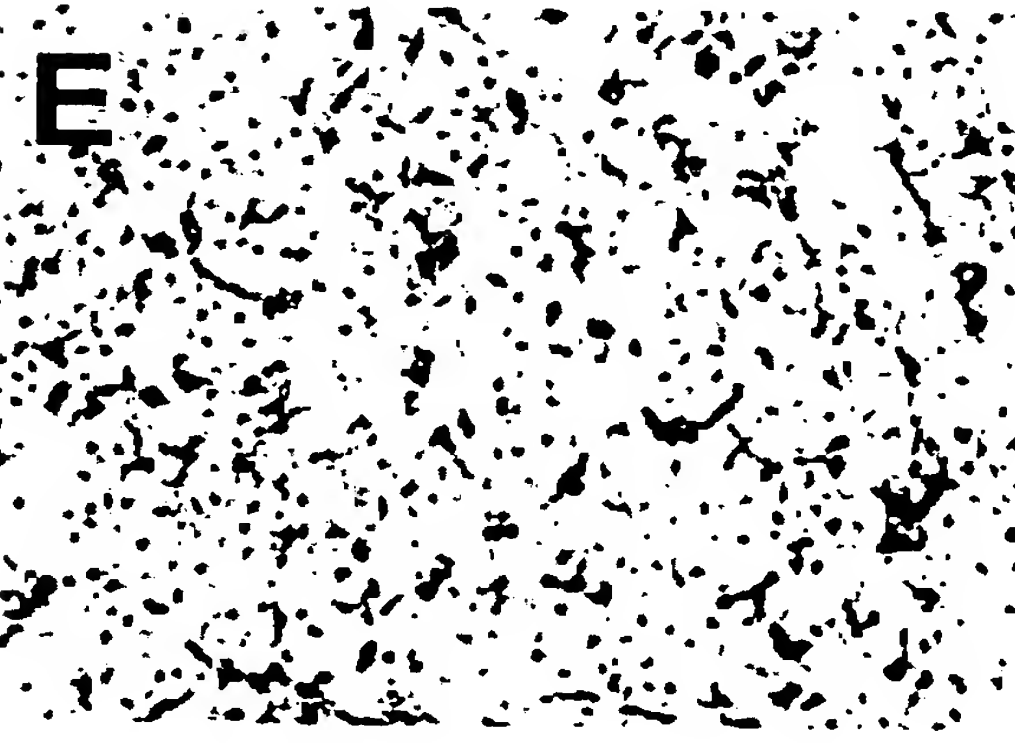
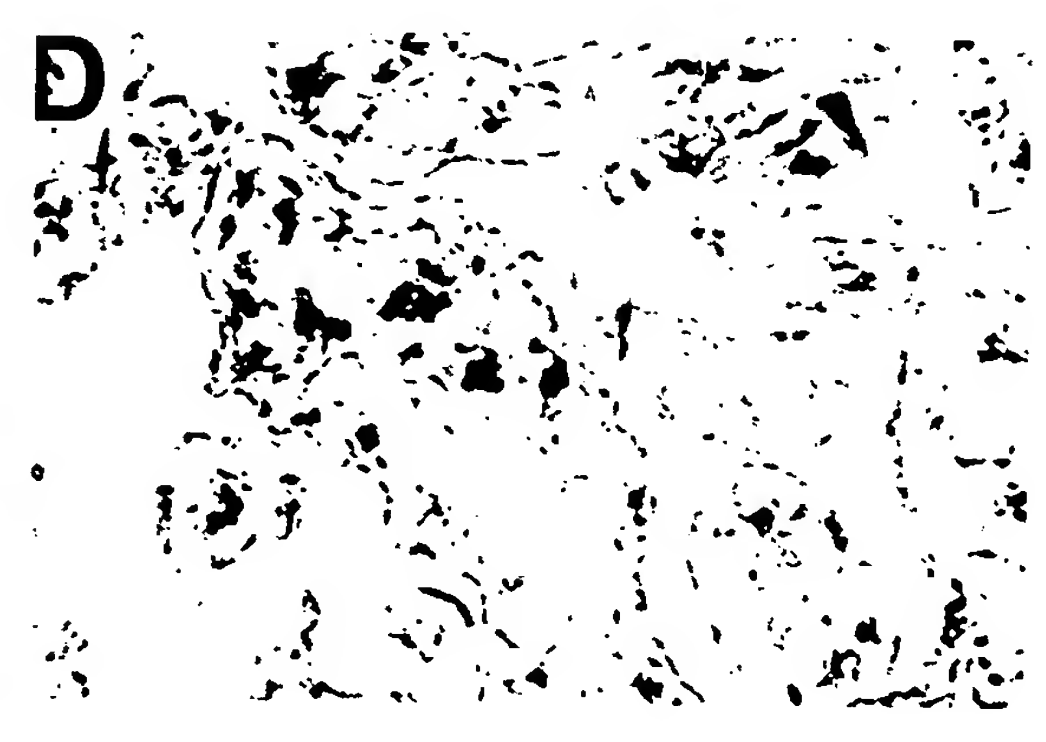
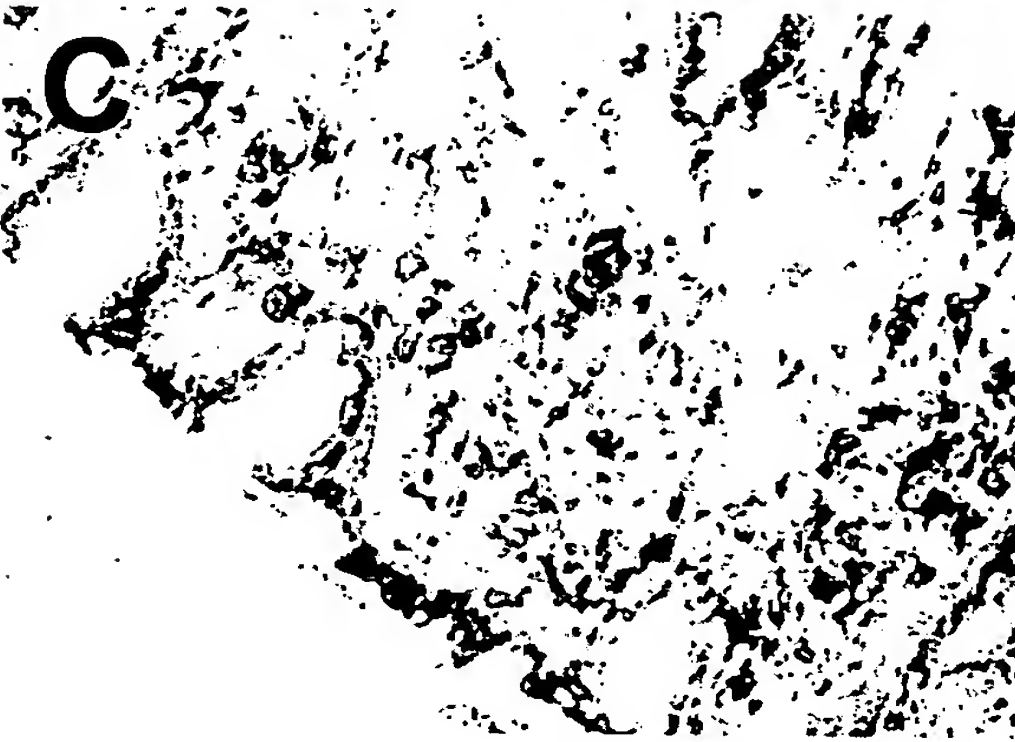
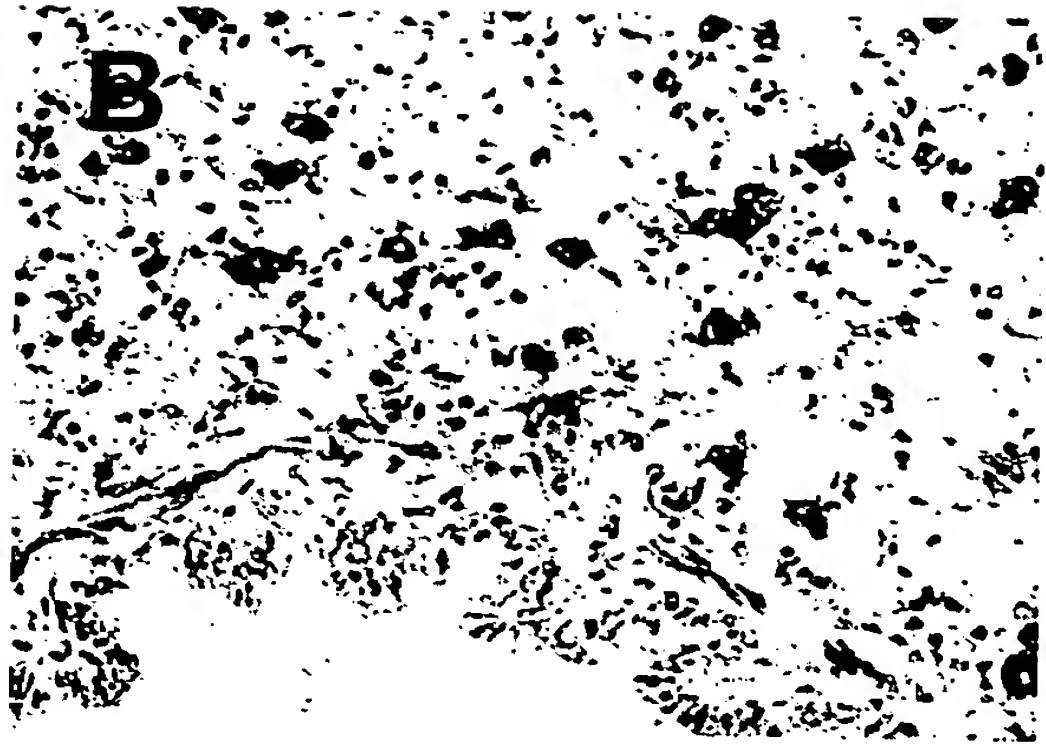
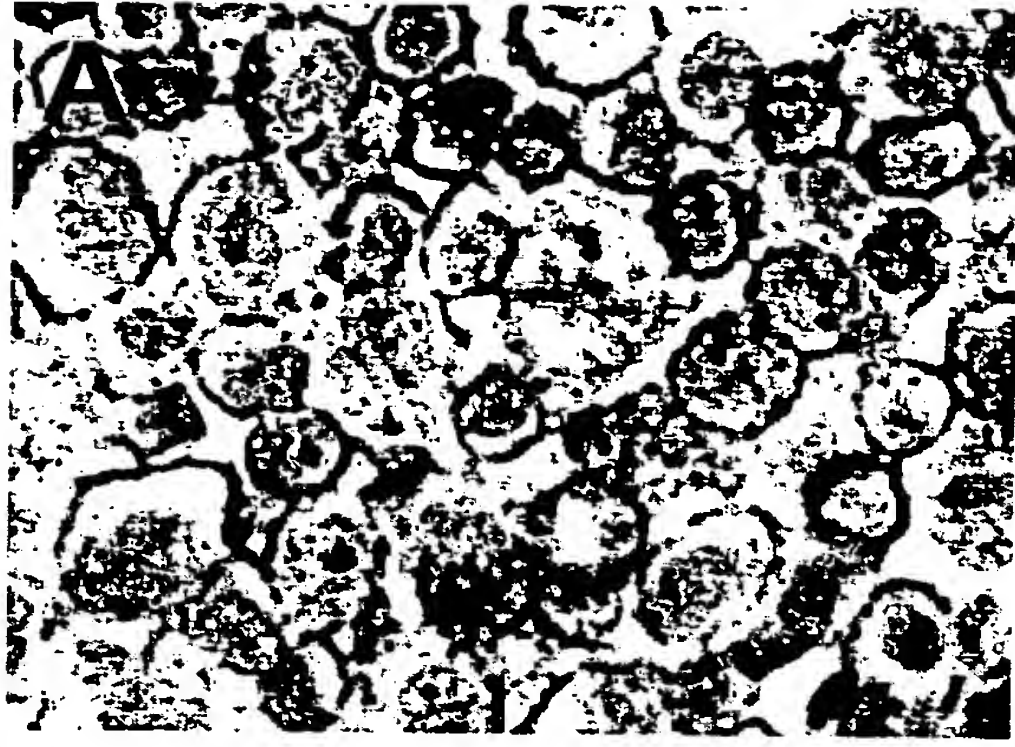


Fig. 66

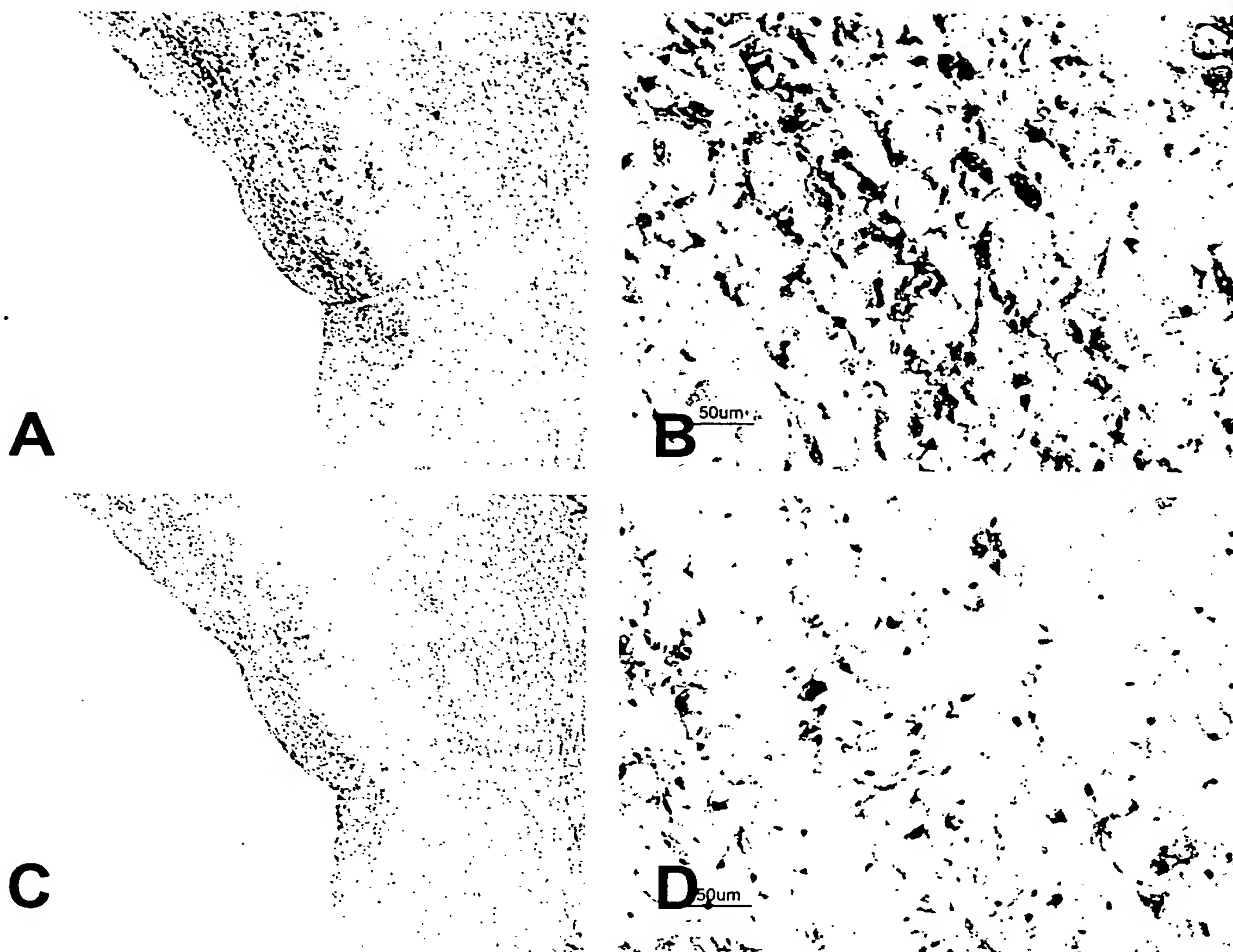


Fig. 67

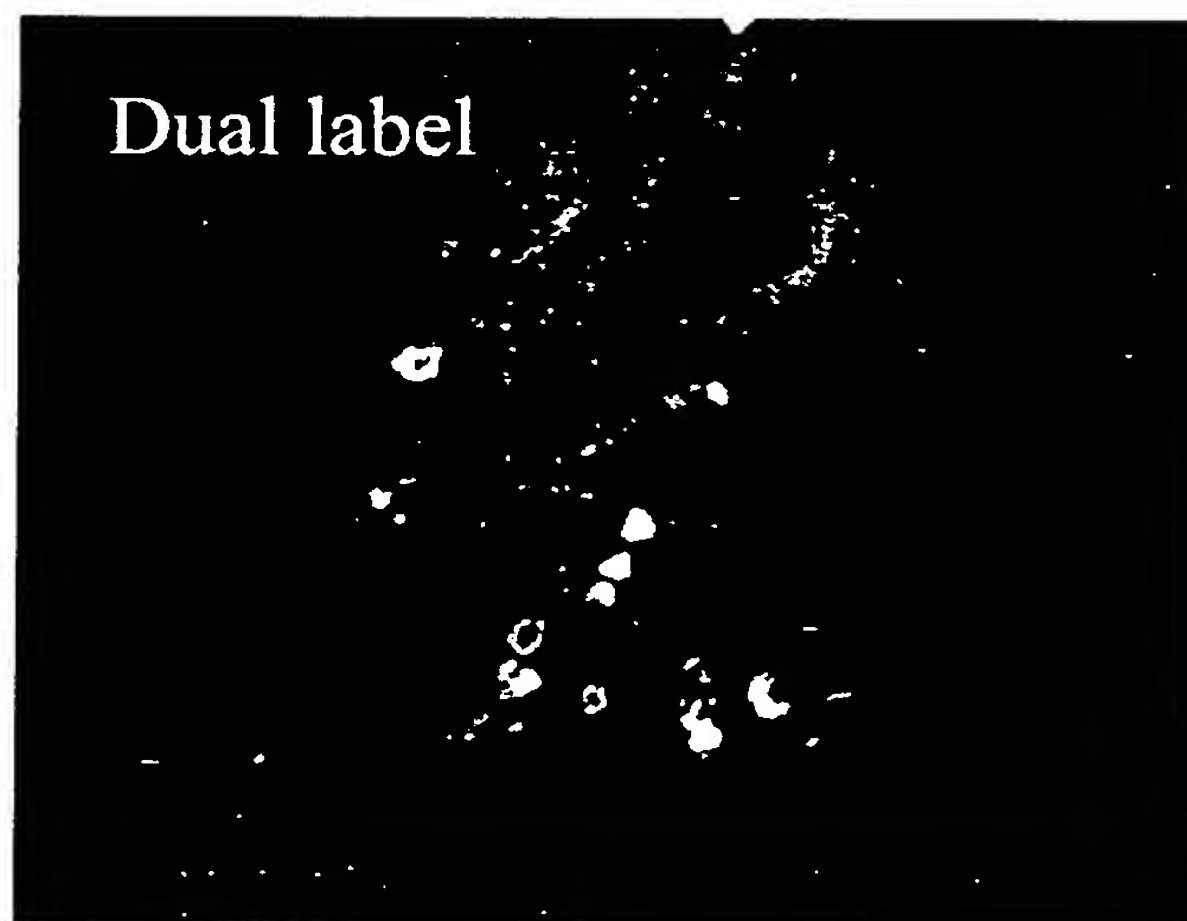
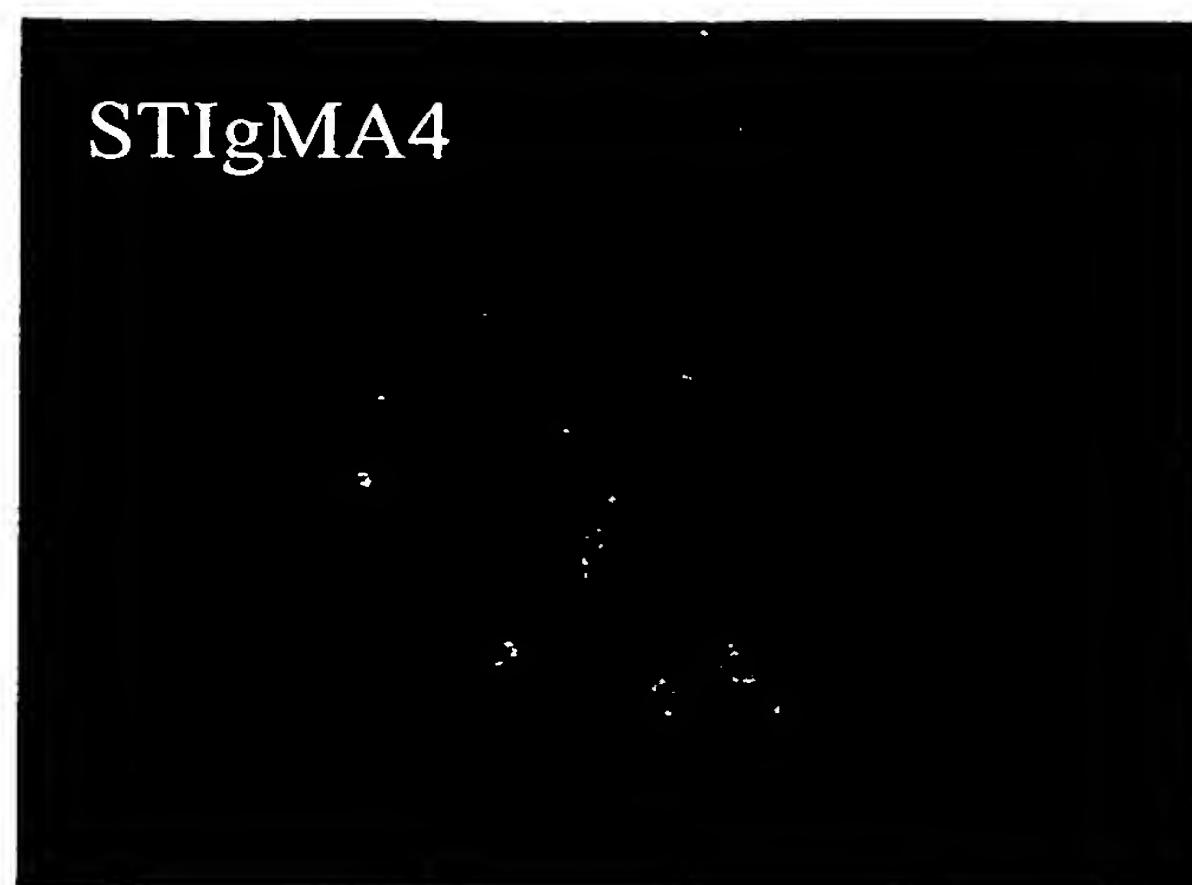


Fig. 68

Fold Difference from normal

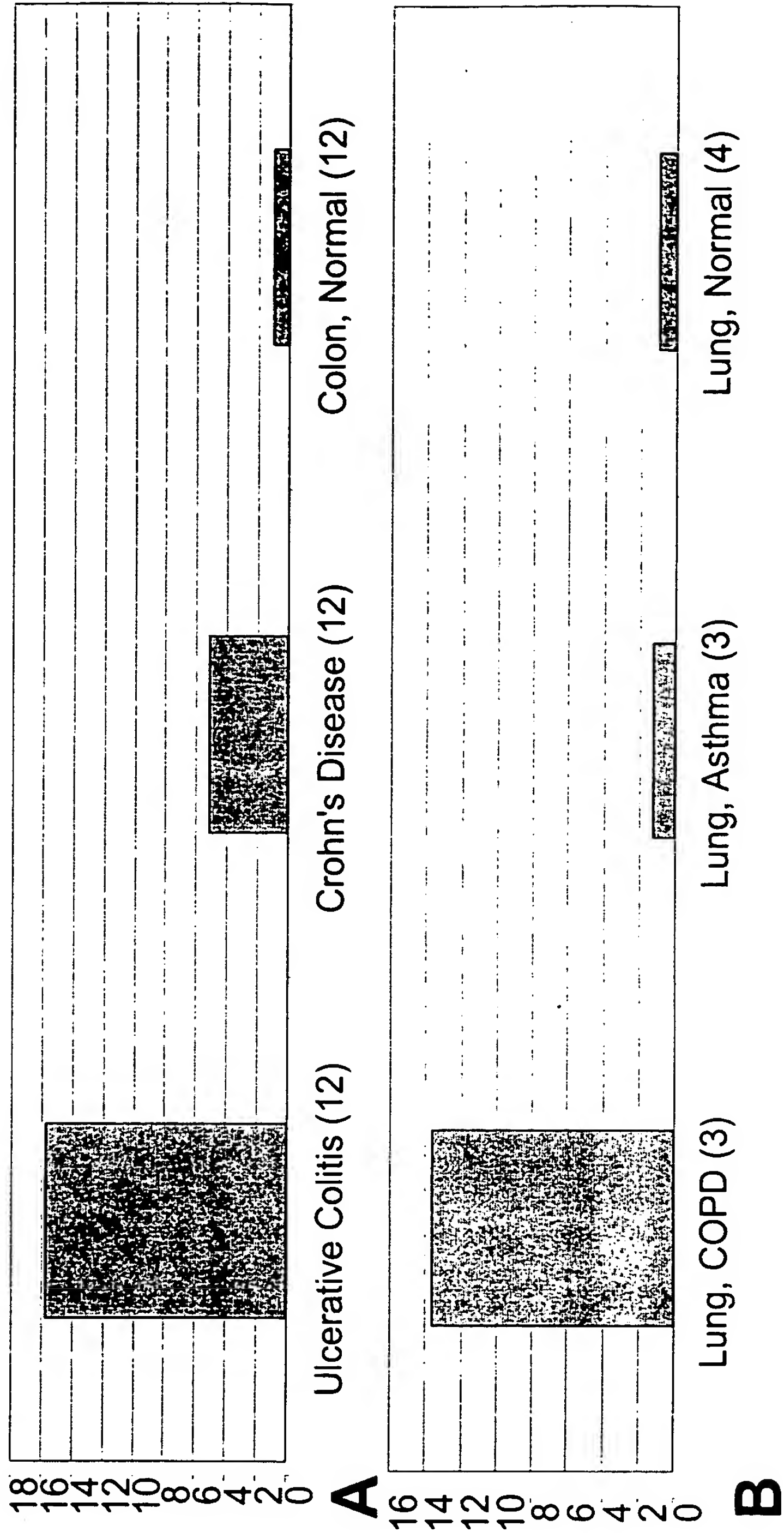
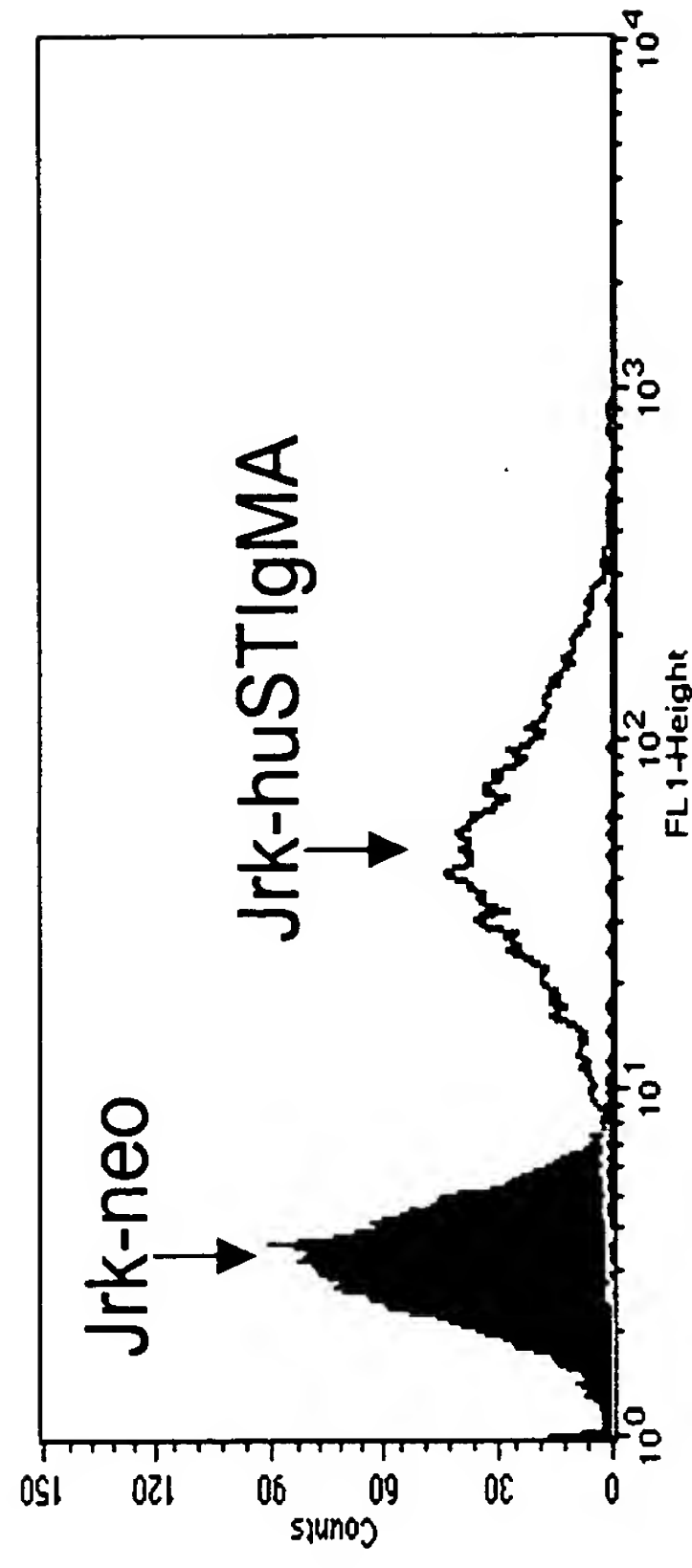
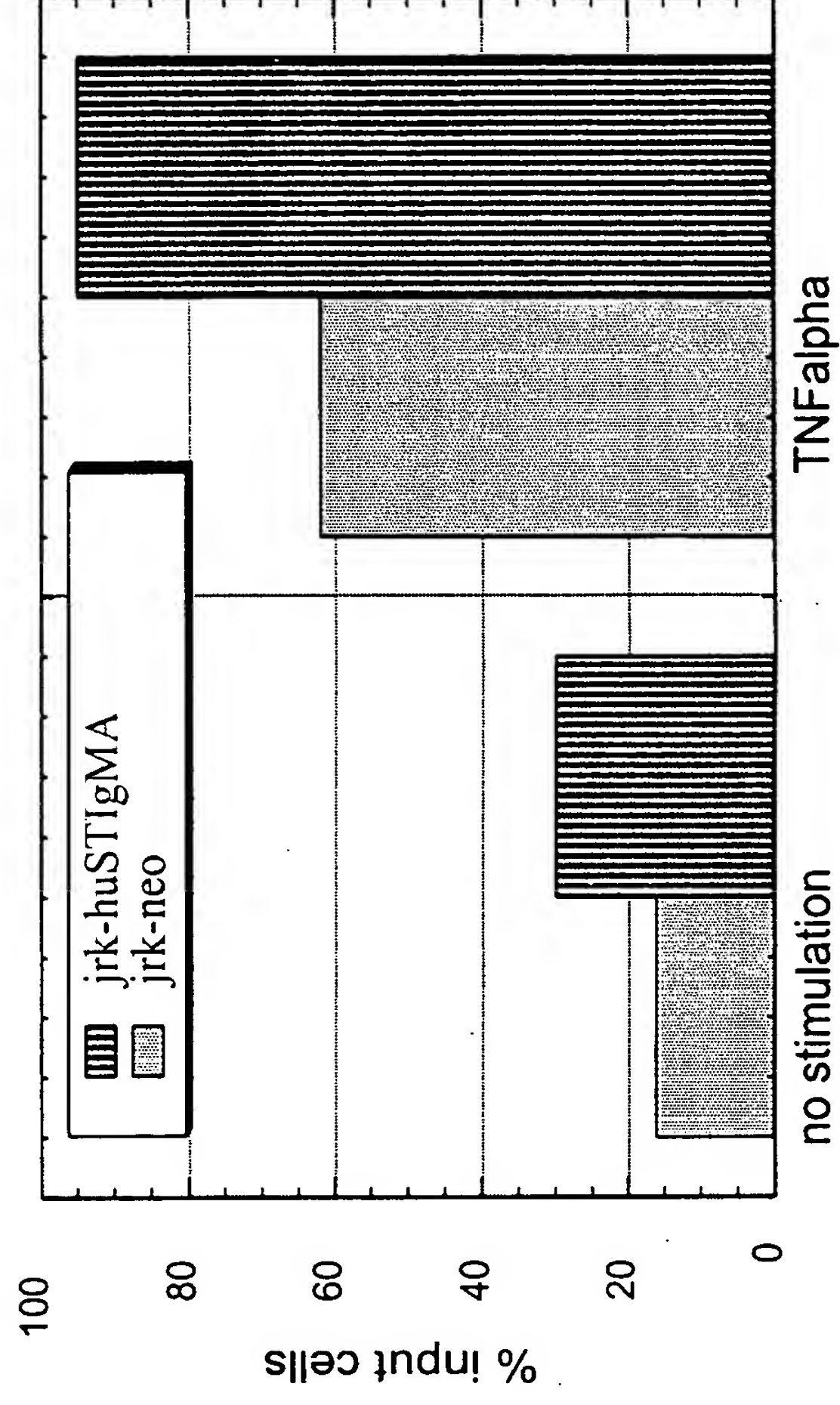


Fig 69



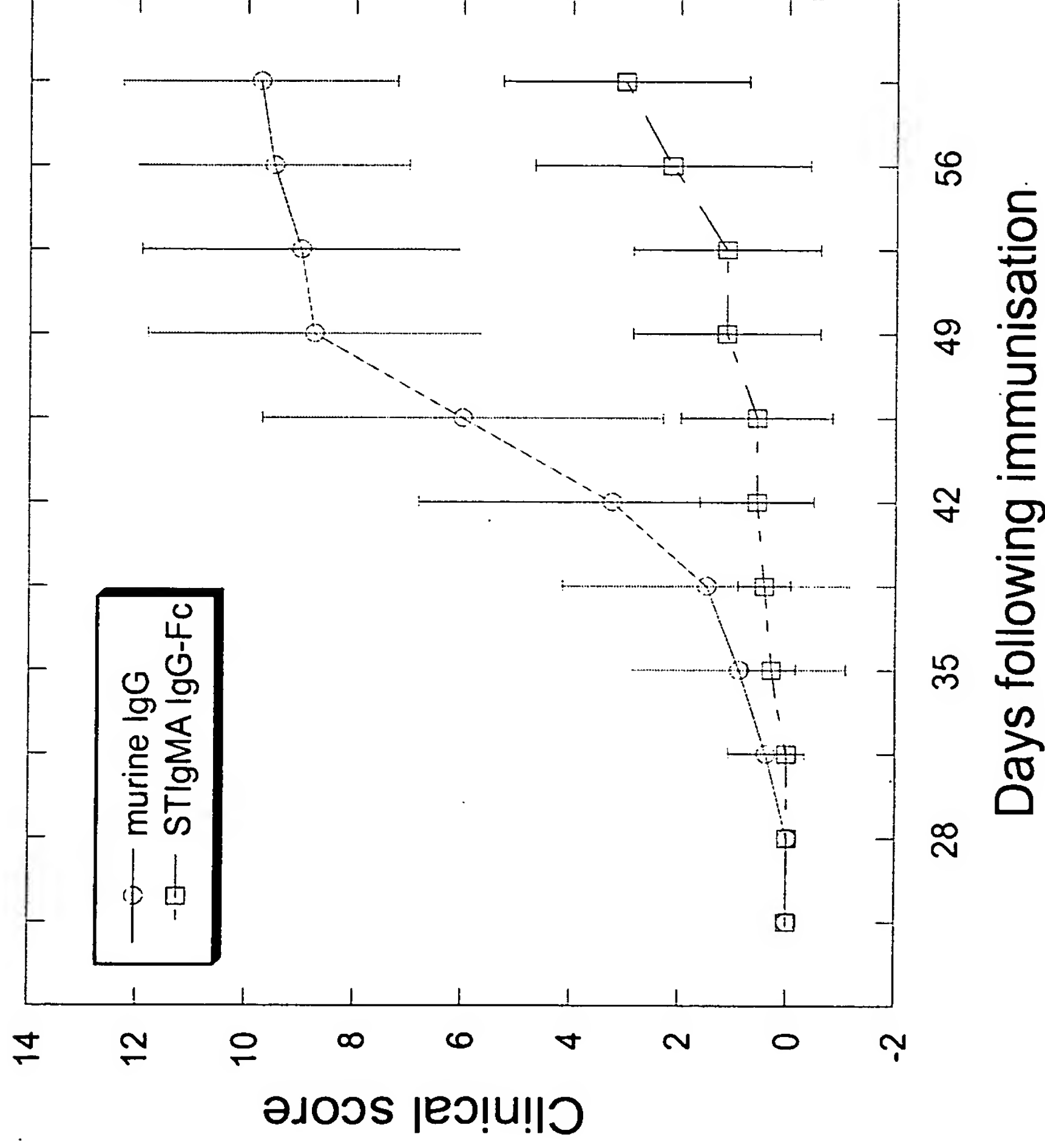
A



B

Fig 70

Figure 71: Effect of Systemic Injection of muSTIgMA-Fc on the Progression of CIA



t-test

p-value = .0004 for IgG1 vs. muSTIgMA

This p-value has been (very) conservatively adjusted for multiple comparisons (Bonferroni adjustment: 2*p-value since there are two comparisons being performed)

Plots indicate mean \pm SD